

SEQ ID	Start	Stop	Score	Direction	Description
11243	294	356	4690	for	Zinc finger, C2H2 type
11244	1	234	8981	for	C2 domain (prot. kinase C like)
11255	66	164	6390	for	WD domain, G-beta repeats
11279	222	377	8686	for	LIM domain containing proteins
11284	69	257	5221	for	Basic region plus leucine zipper transcription factors
11299	42	140	7130	for	WD domain, G-beta repeats
11305	243	398	8736	for	LIM domain containing proteins
11329	222	350	10553	for	Trypsin
11336	8	354	6073	for	Protein Tyrosine Phosphatase
11373	49	209	3996	for	Basic region plus leucine zipper transcription factors
11383	4	180	4978	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
11397	54	437	5176	for	protein kinase
11415	241	520	3929	for	Helicases conserved C-terminal domain
11415	40	612	5187	for	protein kinase
11422	154	216	4870	for	Zinc finger, C2H2 type
11433	2	252	4662	for	RNA recognition motif. (aka RRM, RBD, or RNP domain)
11446	156	212	3520	for	Zinc finger, C2H2 type
11457	9	635	11087	for	wnt family of developmental signaling proteins
11459	289	471	4107	for	Basic region plus leucine zipper transcription factors
11468	200	391	4118	for	Basic region plus leucine zipper transcription factors
11475	163	354	3958	for	Basic region plus leucine zipper transcription factors
11476	207	398	4038	for	Basic region plus leucine zipper transcription factors
11482	107	298	3978	for	Basic region plus leucine zipper transcription factors
11541	180	365	4022	for	Basic region plus leucine zipper transcription factors
11549	100	291	3998	for	Basic region plus leucine zipper transcription factors

SEQ ID	Start	Stop	Score	Direction	Description
11593	196	258	4880	for	Zinc finger, C2H2 type
11595	9	86	6610	for	Homeobox Domain
11596	316	369	5780	rev	Thioredoxins
11607	109	410	17414	for	Ras family
11623	184	372	3977	for	Basic region plus leucine zipper transcription factors
11626	92	439	24100	rev	Phosphatidylinositol-specific phospholipase C, Y domain
11630	263	361	6400	for	WD domain, G-beta repeats
11663	238	433	10572	rev	Serine carboxypeptidases
11674	281	367	2580	for	EF-hand
11681	236	334	5880	for	WD domain, G-beta repeats
11698	64	126	4790	for	Zinc finger, C2H2 type
11720	295	351	4030	for	Zinc finger, C2H2 type
11723	301	378	3460	for	Ank repeat
11727	36	161	4170	for	Basic region plus leucine zipper transcription factors
11730	184	315	8390	for	N-terminal homology in Ets domain
11733	127	294	10770	for	Bromodomain (conserved sequence found in human, Drosophila and yeast proteins.)
11737	9	146	4741	for	Double-stranded RNA binding motif
11738	278	355	3460	for	Ank repeat
11739	123	299	12150	for	Homeobox Domain
11740	127	303	12180	for	Homeobox Domain
11749	184	267	4270	for	Ank repeat
11751	18	173	8987	for	SH3 Domain
11754	51	206	8987	for	SH3 Domain
11758	224	307	4270	for	Ank repeat
11765	12	398	36700	for	G-protein alpha subunit
11828	160	258	6370	for	WD domain, G-beta repeats
11830	35	151	9335	for	Zinc finger, C3HC4 type (RING finger)
11899	60	197	7917	for	Zinc finger, C3HC4 type (RING finger)
11984	253	306	5410	for	Zinc finger, CCHC class
12054	2	401	10596	for	ATPases Associated with Various Cellular Activities

SEQ ID	Start	Stop	Score	Direction	Description
12135	90	179	5380	for	WW/rsp5/WWP domain containing proteins
12137	127	225	5500	for	WD domain, G-beta repeats
12200	20	387	6044	for	Protein Tyrosine Phosphatase
12201	183	353	5136	for	C2 domain (prot. kinase C like)
12205	12	382	5228	for	protein kinase
12229	20	371	5962	for	Protein Tyrosine Phosphatase
12282	48	211	4132	for	Basic region plus leucine zipper transcription factors
12343	43	194	3996	for	Basic region plus leucine zipper transcription factors
12347	25	350	4675	for	Dual specificity phosphatase, catalytic domain
12481	18	101	4560	for	Ank repeat
12496	0	311	10295	for	4 transmembrane segments integral membrane proteins
12510	60	165	4560	for	SH2 Domain
12603	9	461	5759	for	ATPases Associated with Various Cellular Activities
12745	116	400	16107	for	DEAD and DEAH box helicases
12778	100	320	5550	rev	ATPases Associated with Various Cellular Activities
12790	198	392	9384	for	DEAD and DEAH box helicases
12863	18	281	10480	for	Calpain large subunit, domain III
12888	5	387	5976	rev	protein kinase
12934	131	214	3600	for	Ank repeat
12966	191	292	5295	for	WD domain, G-beta repeats
13000	190	252	4360	for	Zinc finger, C2H2 type
13027	275	367	5791	for	WD domain, G-beta repeats
13066	190	369	4022	for	Basic region plus leucine zipper transcription factors
13071	129	320	3947	for	Basic region plus leucine zipper transcription factors
13077	167	334	4180	for	Basic region plus leucine zipper transcription factors
13094	14	164	5951	for	mkk like kinases
13094	8	112	5968	for	protein kinase
13097	45	386	19398	for	ATPases Associated with Various Cellular Activities
13102	14	215	9133	for	4 transmembrane segments integral membrane proteins
13109	229	390	6089	for	mkk like kinases
13109	118	390	8063	for	protein kinase
13112	293	355	3570	for	Zinc finger, C2H2 type

SEQ ID	Start	Stop	Score	Direction	Description
13114	0	215	10146	for	4 transmembrane segments integral membrane proteins
13116	281	343	4490	for	Zinc finger, C2H2 type
13127	34	256	4190	for	Basic region plus leucine zipper transcription factors
13177	138	394	9877	for	Ras family
13185	8	139	9328	for	ATPases Associated with Various Cellular Activities
13186	97	180	3820	for	Ank repeat
13193	11	187	15442	for	Fork head domain, eukaryotic transcription factors
13200	15	182	9681	for	mkk like kinases
13204	16	102	4680	for	EF-hand
13211	208	300	5585	for	WD domain, G-beta repeats
13216	7	153	6100	for	Helicases conserved C-terminal domain
13225	161	223	4900	for	Zinc finger, C2H2 type
13226	43	321	8740	for	SH2 Domain
13258	94	342	14970	for	SH2 Domain
13264	65	271	12512	for	PDZ domain
13270	124	270	6068	for	Phorbol esters/diacylglycerol binding

Example 58

DIFFERENTIAL EXPRESSION OF POLYNUCLEOTIDES OF THE INVENTION:

DESCRIPTION OF LIBRARIES AND DETECTION OF DIFFERENTIAL EXPRESSION

- 5 The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 88 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepare the cDNA library, the abbreviated name of the library that is used in the tables below (in quotes), and the approximate number
- 10 of clones in the library.

Table 88

Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in this Clustering
1	Km12 L4 Human Colon Cell Line, High Metastatic Potential (derived from Km12C) "High Colon"	307133
2	Km12C Human Colon Cell Line, Low Metastatic Potential "Low Colon"	284755
3	MDA-MB-231 Human Breast Cancer Cell Line, High Metastatic Potential; micro-metastases in lung "High Breast"	326937
4	MCF7 Human Breast Cancer Cell, Non Metastatic "Low Breast"	318979
8	MV-522 Human Lung Cancer Cell Line, High Metastatic Potential "High Lung"	223620
9	UCP-3 Human Lung Cancer Cell Line, Low Metastatic Potential "Low Lung"	312503
12	Human microvascular endothelial cells (HMEC) – Untreated PCR (OligodT) cDNA library	41938

Library (lib #)	Description	Number of Clones in this Clustering
13	Human microvascular endothelial cells (HMEC) – Basic fibroblast growth factor (bFGF) treated PCR (OligodT) cDNA library	42100
14	Human microvascular endothelial cells (HMEC) – Vascular endothelial growth factor (VEGF) treated PCR (OligodT) cDNA library	42825
15	Normal Colon – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	34285
16	Colon Tumor – UC#2 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	35625
17	Liver Metastasis from Colon Tumor of UC#2 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	36984
18	Normal Colon – UC#3 Patient PCR (OligodT) cDNA library “Normal Colon Tumor Tissue”	36216
19	Colon Tumor – UC#3 Patient PCR (OligodT) cDNA library “High Colon Tumor Tissue”	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient PCR (OligodT) cDNA library “High Colon Metastasis Tissue”	30956
21	G RRpz Human Prostate Cell Line	164801
22	WOca Human Prostate Cancer Cell Line	162088

The KM12L4 and KM12C cell lines are described in Example 55 above. The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-

recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., *Int J Cancer* (1987) 40:46 (UCP-3); Varki et al., *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki et al., *Anticancer Res.* (1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz cell line refers to low passage (3 passages or fewer) human prostate cells, and the WOca cell line refers to low passage (3 passages or fewer) human prostate cancer cells.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac et al., *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same

cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 5 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones 10 corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) 15 dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed 20 between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974)).

25

EXAMPLE 59

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL BREAST CANCER CELLS VERSUS LOW METASTATIC BREAST CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially 30 expressed between cells derived from high metastatic potential breast cancer tissue and low metastatic breast cancer cells. Expression of these sequences in breast cancer can be valuable in determining diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process.

A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential breast cancer cells and low metastatic potential breast cancer cells.

Table 89

Differentially expressed polynucleotides: Higher expression in high metastatic potential breast cancer (lib3) relative to low metastatic breast cancer cells (lib4)

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
472	64	0	62
11770	6	0	6
11775	8	0	8
11786	6	0	6
11791	6	0	6
11794	12	3	4
11842	89	22	4
12037	7	0	7
12038	7	0	7
12054	37	13	3
12109	19	0	19
12112	16	5	3
12151	12	2	6
12158	6	0	6
12257	21	2	10
12297	16	4	4
12313	6	0	6
12314	6	0	6
12409	13	3	4
12424	16	2	8
12459	8	1	8

SEQ ID NOs:	Lib3 clones	Lib4 clones	lib3/lib4
12461	11	1	11
12526	11	2	5
12559	22	5	4
12593	8	0	8
12598	19	0	19
12603	14	4	3
12626	8	0	8
12643	9	0	9
12676	6	0	6
12695	10	0	10
12723	13	2	6
12737	6	0	6
12825	14	0	14
12878	26	8	3
12883	17	4	4
12887	6	0	6
12896	22	3	7
12899	13	1	13
12929	6	0	6
12962	10	1	10
12990	33	12	3
12991	9	1	9
13014	19	3	6
13016	11	2	5
13092	12	2	6
13122	8	1	8
13129	27	8	3
13131	13	1	13
13203	8	0	8
13207	6	0	6
13250	14	3	5
13254	13	1	13

Table 90

Differentially expressed polynucleotides: Higher expression in low metastatic breast cancer cells (lib4) relative to high metastatic potential breast cancer (lib3)

5

SEQ ID NOs:	Lib 3 Clones	Lib 4 Clones	lib4/lib3
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10321	0	6	6
10533	3	21	7
10543	0	6	6
10545	0	8	8
10631	0	9	9
10663	0	7	7
11244	2	29	15
11371	2	13	7
11799	0	9	9
11834	0	7	7
11870	0	6	6
11874	8	32	4
11934	0	7	7
11965	0	7	7
11995	1	22	23
12006	0	6	6
12043	0	9	9
12064	0	8	8
12081	0	6	6
12082	0	12	12
12083	5	19	4
12091	2	15	8
12111	5	16	3
12163	20	43	2
12185	3	18	6
12232	24	56	2
12265	1	13	13
12274	0	10	10
12290	0	6	6
12312	1	17	17
12323	1	21	22
12362	0	6	6
12379	0	11	11
12442	0	6	6
12494	1	10	10
12497	0	6	6
12503	1	17	17
12509	0	6	6
12528	1	9	9

12551	5	24	5
12633	5	24	5
12647	0	6	6
12671	1	14	14
12713	4	15	4
12745	0	7	7
12906	5	15	3
12924	1	14	14
12928	20	58	3
12966	4	17	4
12976	2	17	9
12994	2	11	6
12995	0	6	6
13021	0	6	6
13047	15	52	4
13051	15	52	4
13061	0	6	6
13106	22	49	2
13172	23	96	4
13201	19	46	2
13204	20	40	2
13265	0	9	9

5

EXAMPLE 60

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL LUNG
CANCER CELLS VERSUS LOW METASTATIC LUNG CANCER CELLS

10 A number of polynucleotide sequences have been identified that are differentially
expressed between cells derived from high metastatic potential lung cancer cells and low
metastatic lung cancer cells. Expression of these sequences in lung cancer tissue can be
valuable in determining diagnostic, prognostic and/or treatment information. For example,
sequences that are highly expressed in the high metastatic potential cells can be indicative
of increased expression of genes or regulatory sequences involved in the metastatic process.

A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential lung cancer cells and low metastatic potential lung cancer cells:

Table 91

Differentially expressed polynucleotides: Higher expression in high metastatic potential lung cancer cells (lib8) relative to low metastatic lung cancer cells (lib9)

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
9933	10	0	10
10056	5	0	5
10070	5	0	7
10071	9	0	13
10090	6	0	8
10119	10	0	14
10173	5	0	7
10181	5	0	7
10190	5	0	7
10267	6	1	8
10331	5	0	7
10426	5	0	7
10439	6	0	8
10449	5	0	7
10507	5	0	7
10542	7	0	10
10556	7	0	10
10579	5	0	7
10597	8	0	11
10599	5	0	7
10619	9	2	6

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
10633	28	13	3
10693	11	0	15
10731	5	0	7
10753	8	2	6
10820	11	2	8
11087	5	0	7
11252	6	0	8
11271	5	0	7
11443	11	1	15
11625	5	0	7
11671	17	9	3
11687	20	4	7
11688	5	0	7
11699	6	0	8
11700	40	3	19
11718	6	1	8
11722	6	1	8
11730	16	9	2
11803	6	0	8
11838	8	1	11
11858	6	0	8
11894	43	9	7
11943	12	1	17
11964	8	1	11
11979	20	13	2
11990	16	4	6
12047	5	0	7
12096	10	2	7
12100	44	13	5
12103	11	1	15
12104	10	4	3
12202	7	0	10
12230	10	4	3
12233	10	0	14
12312	14	6	3
12317	6	1	8
12379	10	4	3
12433	6	0	8
12516	5	0	7
12576	8	2	6
12588	6	1	8
12589	6	1	8
12966	21	3	10
12969	16	5	4

SEQ ID NO:	Lib8 clones	Lib9 clones	lib8/lib9
13011	7	1	10
13059	181	119	2
13076	5	0	7
13106	16	5	4
13129	5	0	7
13139	28	4	10
13155	7	1	10
13168	16	0	22
13183	8	2	6
13224	7	0	10
13228	20	0	28
13237	24	4	8
13249	5	0	7
13250	5	0	7

Table 92

Differentially expressed polynucleotides: Higher expression in low metastatic lung cancer cells (lib 9) relative to high metastatic potential lung cancer cells (lib 8)

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
9943	3	20	5
9972	0	18	13
9983	0	8	6
9989	0	11	8
10024	10	66	5
10048	0	16	11
10133	1	14	10
10152	4	35	6
10156	0	13	9
10183	0	29	21
10248	2	17	6
10287	1	37	26
10289	0	11	8
10337	0	8	6
10369	0	9	6
10380	0	9	6
10403	0	26	19
10413	0	41	29
10436	1	12	9
10441	1	11	8
10500	1	17	12

SEQ ID NO:	Lib 8 clones	Lib 9 clones	lib 9/lib 8
10533	3	23	5
10625	0	11	8
10645	5	23	3
10725	0	14	10
10743	0	9	6
10755	1	14	10
10793	0	12	9
10819	5	21	3
10936	2	14	5
11063	0	8	6
11073	0	12	9
11085	2	45	16
11089	1	13	9
11221	2	13	5
11245	1	13	9
11246	1	13	9
11286	0	12	9
11296	0	12	9
11356	2	18	6
11361	1	14	10
11385	0	13	9
11395	0	13	9
11414	0	8	6
11415	1	13	9
11583	38	253	5
11601	1	17	12
11606	0	9	6
11677	0	8	6
11736	4	18	3
11756	3	16	4
11764	3	23	5
11775	2	17	6
11829	1	18	13
12065	2	16	9
12075	0	9	6
12382	0	12	9
12643	10	38	3
12668	403	2000	4
12720	6	25	3
12912	3	18	4
12999	0	10	7
13026	3	23	5
13211	0	20	14
13243	110	548	4

EXAMPLE 61

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL COLON
CANCER CELLS VERSUS LOW METASTATIC COLON CANCER CELLS

5

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer cells and low metastatic colon cancer cells. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the metastatic process. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment. In another example, sequences that display higher expression in the low metastatic potential cells can be associated with genes or regulatory sequences that inhibit metastasis, and thus the expression of these polynucleotides in a sample may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

Table 93

Differentially expressed polynucleotides: Higher expression in low metastatic colon cancer cells (lib 2) relative to high metastatic potential colon cancer cells (lib 1)

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
10348	0	9	10
11413	0	8	9
11842	34	114	4
11905	3	12	4
11937	0	9	10
11955	2	10	5
11968	8	25	3

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
12054	24	87	4
12065	2	16	9
12127	6	27	5
12134	2	11	6
12158	1	10	11
12226	2	12	6
12232	28	62	2
12276	5	14	3
12279	3	21	8
12281	0	6	6
12297	3	12	4
12488	3	20	7
12490	0	6	6
12507	54	172	3
12511	15	41	3
12530	0	6	6
12555	0	9	10
12560	7	20	3
12569	0	9	10
12581	0	9	10
12593	4	13	4
12601	0	6	6
12621	9	25	3
12623	8	23	3
12634	2	12	6
12723	9	22	3
12740	13	29	2
12759	1	8	9
12765	2	15	8
12785	0	6	6
12825	0	6	6
12834	44	109	3
12852	0	6	6
12854	5	16	3
12876	1	11	12
12878	3	27	10
12896	16	30	2
12899	12	27	2
12919	2	13	7
12928	12	29	3
13034	0	7	8
13075	502	2170	5
13129	2	21	11
13130	0	9	10

SEQ ID NOs:	Lib 1 clones	Lib 2 clones	lib 2/lib 1
13132	0	7	8
13154	2	12	6
13170	2	12	6
13215	3	12	4
13254	1	8	9

EXAMPLE 62

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH METASTATIC POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

5

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high metastatic potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information. For example, sequences that are highly expressed in the high metastatic potential cells can be indicative of increased expression of genes or regulatory sequences involved in the advanced disease state which involves processes such as angiogenesis, dedifferentiation, cell replication, and metastasis. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant more aggressive treatment.

15 The differential expression of these polynucleotides can be used as a diagnostic marker, a prognostic marker, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

20 The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer tissue and normal colon tissue:

Table 94

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3 and) : Lower expression in high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20) vs. normal colon tissue (patient 2:lib 15; patient 3:lib 18)

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
9988	19	7	3
10042	6	0	6
10059	24	8	3

SEQ ID NO:	lib 15 clones	lib 17 clones	lib 15/lib 17
10116	6	0	6
10117	113	0	121
10173	28	9	3
10331	28	9	3
10431	11	1	12
10560	17	7	3
10561	7	0	8
10873	12	3	4
10930	209	16	14
10943	8	0	9
10959	12	3	4
10974	26	7	4
11025	31	15	2
11044	17	0	18
11048	17	0	18
11057	109	0	117
11163	14	1	15
11172	73	0	78
11202	34	7	5
11204	34	7	5
11258	13	4	3
11393	73	0	78
11424	18	3	6
11472	68	6	12
11473	2542	14	195
11524	2542	14	195
11547	6	0	6
11562	142	4	38
11672	12	0	10
11683	13	0	14
SEQ ID NO:	Lib18 Clones	Lib20 Clones	lib18/lib20
10024	28	11	2
10117	21	0	18
10173	9	0	8
10331	9	0	8
10930	11	1	9
11057	14	0	12
11172	23	0	20
11562	18	0	15
11683	12	0	10
13075	140	43	3

Table 95

Differentially expressed polynucleotides isolated from samples from two patients (patient 2 and patient 3): Lower expression in normal colon tissue (patient 2:lib 15; patient 3:lib 18)vs. high metastatic potential colon tissue (patient 2:lib 17; patient 3:lib 20).

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
10240	3	23	7
10282	1	9	8
10755	21	99	4
10778	6	20	3
10804	13	28	2
10835	13	28	2
10900	2	11	5
11145	8	70	8
11227	0	8	7
11236	29	84	3
11348	27	127	4
11361	0	9	8
11453	1	12	11
11459	12	43	3
11471	0	7	7
11475	1	9	8
11476	1	9	8
11488	2189	5122	2
11490	6	18	3
11495	3	25	8
11500	4	22	5
11520	25	157	6
11532	9	48	5
11535	15	61	4
11539	2	17	8
11541	4	99	23
11545	6	35	5
11566	4	22	5
11583	4	28	7
11602	2	18	8
11623	3	15	5
11719	0	7	7
12668	23	60	2
12703	4	14	3
12724	1	9	8
12895	3	14	4
13047	18	57	3
13048	26	124	4

SEQ ID NO:	Lib 15 Clones	Lib 17 Clones	lib 17/lib 15
13065	64	210	3
13069	940	2267	2
13070	2	15	7
SEQ ID NO:	lib 18 clones	lib 20 clones	lib 20/lib 18
10784	0	5	6
11488	1	7	8
11499	1	7	8
11509	1	7	8
12709	0	5	6

EXAMPLE 63

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH COLON TUMOR POTENTIAL PATIENT TISSUE VERSUS METASTASIZED COLON CANCER PATIENT TISSUE

5 A number of polynucleotide sequences have been identified that are differentially
expressed between cells derived from colon cancer tissue and cells derived from colon
cancer tissue metastases to liver. Expression of these sequences in colon cancer tissue can
provide diagnostic, prognostic and/or treatment information associated with the
transformation of precancerous tissue to malignant tissue. This information can be useful
10 in the prevention of achieving the advanced malignant state in these tissues, and can be
important in risk assessment for a patient.

The following table summarizes identified polynucleotides with differential
expression between high tumor potential colon cancer tissue and cells derived from high
metastatic potential colon cancer cells:

15

Table 96

Differentially expressed polynucleotides:
Greater expression in metastatic colon tumor tissue (lib 20) vs.
colon tumor tissue (lib 19)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 20/lib 19
10856	0	6	8
10895	0	5	7
11439	1	8	11
11465	1	11	15
11469	1	11	15
11493	1	8	11
11499	0	7	9
11509	0	7	9
11518	8	21	4
11526	158	632	5
11541	1	7	9

5

Table 97

Greater expression in colon tumor tissue (lib 19) than metastatic colon tissue (lib 20)

SEQ ID NO:	lib 19 clones	lib 20 clones	lib 19/lib 20
10024	64	11	4
10930	53	1	40
11145	18	4	3
11490	8	0	6
11645	15	3	4
11730	17	2	6
12668	47	6	6
13065	19	2	7
13243	20	1	15

EXAMPLE 64

10

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN HIGH TUMOR POTENTIAL
COLON CANCER PATIENT TISSUE VERSUS NORMAL PATIENT TISSUE

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from high tumor potential colon cancer tissue and normal tissue. Expression of these sequences in colon cancer tissue can provide diagnostic,

prognostic and/or treatment information associated with the prevention of the malignant state in these tissues, and can be important in risk assessment for a patient. For example, sequences that are highly expressed in the potential colon cancer cells are associated with or can be indicative of increased expression of genes or regulatory sequences involved in early tumor progression. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following tables summarize polynucleotides that are differentially expressed between high metastatic potential colon cancer cells and normal colon cells:

10

Table 98

Differentially expressed polynucleotides detected in samples from patient (patient 2)
Higher expression in normal colon tissue (patient 2, lib 15)
vs. tumor potential colon tissue (patient 2:lib16)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
9988	19	7	3
10024	116	54	2
10059	24	4	6
10116	6	0	6
10117	113	3	40
10173	28	6	5
10331	28	6	5
10561	7	0	7
10749	10	2	5
10857	31	13	3
10930	209	37	6
11014	12	3	4
11044	17	0	18
11048	17	0	18
11057	109	1	115
11172	73	1	77
11202	34	13	3
11204	34	13	3
11258	13	3	5
11372	11	3	4
11393	73	1	77
11424	18	6	3
11473	2542	448	6
11524	2542	448	6

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
11533	36	14	3
11549	24	9	3
11562	142	2	75
11565	39	14	3
11568	24	8	3
11596	19	6	3
11672	13	0	14
11683	13	0	14
11685	177	65	3
11691	24	8	3

Table 99

Differentially expressed polypeptides detected in samples from patient. Lower expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
13065	3	19	6
13069	21	228	10
13243	3	20	6

Table 100

Differentially expressed polypeptides detected in samples from patient. Higher expression in normal colon tissue (lib 18) than colon tumor tissue (lib 19)

SEQ ID NO:	lib 18 clones	lib 19 clones	lib 18/lib 19
10117	21	2	12
10384	6	0	7
10408	6	0	7
10664	6	0	7
10778	11	2	6
10895	7	0	8
10930	209	37	6
10964	8	1	9
11057	14	0	16
11172	23	0	26
11311	16	4	5
11393	23	0	26
11508	6	0	7
11510	22	11	2
11526	386	158	3
11562	18	0	21
11672	12	0	14
11683	12	0	14
SEQ ID NO:	lib 18 clones	lib 19 clones	lib 19/lib 18
10024	28	64	2
10930	11	53	4
11145	2	18	8
11170	6	19	3
11478	1	9	8
11490	0	8	7
11527	1	9	8
11685	2	13	6
11701	1	9	8
11730	1	17	15

Table 101

Differentially expressed polynucleotides:

Higher expression in colon tumor tissue

(patient 2, lib 16) vs. normal colon tissue (patient 2, lib 15)

SEQ ID NO:	lib 15 clones	lib 16 clones	lib 16/lib 15
9926	1	9	9
10083	6	19	3
10653	4	15	4
10755	21	53	2
10847	2	11	5
10884	2	11	5
10906	2	11	5
10945	7	19	3
10963	4	16	4
11038	4	16	4
11145	8	46	5
11146	0	9	9
11170	7	95	13
11235	0	6	6
11348	27	81	3
11361	0	9	9
11459	12	28	2
11472	68	590	8
11479	4	24	6
11496	1	10	9
11507	5	20	4
11529	3	13	4
11539	2	23	11
11545	6	23	4
11592	2	15	7
12335	0	7	7
12668	23	54	2
12895	3	14	4
13048	26	64	2
13051	18	54	3

EXAMPLE 65

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN GROWTH FACTOR-STIMULATED HUMAN MICROVASCULAR ENDOTHELIAL CELLS (HMEC) RELATIVE TO UNTREATED HMEC

A number of polynucleotide sequences have been identified that are differentially expressed between human microvascular endothelial cells (HMEC) that have been treated with growth factors relative to untreated HMEC.

Sequences that are differentially expressed between growth factor-treated HMEC and untreated HMEC can represent sequences encoding gene products involved in angiogenesis, metastasis (cell migration), and other developmental and oncogenic processes. For example, sequences that are more highly expressed in HMEC treated with growth factors (such as bFGF or VEGF) relative to untreated HMEC can serve as markers of cancer cells of higher metastatic potential. Detection of expression of these sequences in colon cancer tissue can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

The following table summarizes identified polynucleotides with differential expression between growth factor-treated and untreated HMEC.

Table 102

Differentially expressed polynucleotides:

Higher expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

SEQ ID NO:	lib 12 clones	lib 13 clones	lib 12/lib 13
10768	6	0	6
10978	6	0	6
11125	12	2	6
13127	12	0	12

Lower expression in untreated HMEC (lib 12) vs. bFGF treated HMEC (lib 13)

12667	3	12	4
13244	0	6	6

Table 103

Differentially expressed polynucleotides:

Higher expression in untreated HMEC (lib 12) VEGF treated HMEC (lib14)

SEQ ID NO:	lib 12 clones	lib 14 clones	lib 12/lib 14
11069	9	0	9

5

Lower expression in untreated HMEC (lib 12) vs. VEGF treated HMEC (lib14)

13243	22	50	2
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EXAMPLE 66

10 POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED IN NORMAL PROSTATE CELLS RELATIVE TO PROSTATE CANCER CELLS

A number of polynucleotide sequences have been identified that are differentially expressed between cells derived from normal prostate cells and prostate cancer cells. Expression of these sequences prostate tissue suspected of being cancerous can provide
 15 diagnostic, prognostic and/or treatment information. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers. The following table summarizes identified polynucleotides with differential expression between high metastatic potential colon cancer cells and low metastatic potential colon cancer cells:

20

Table 104

Differentially expressed polynucleotides: normal prostate cell line (lib 21)
 vs. prostate cancer cell line (lib 22)

Higher in lib 21

SEQ ID NO:	lib 21 clones	lib 22 clones	lib 21/lib 22
9972	17	2	8
11673	22	8	3

11720	7	0	7
11764	22	6	4
10365	8	0	8
11329	6	0	6
11979	18	6	3
12062	12	3	4
12551	13	1	13
12818	16	2	8
13257	12	2	6

Higher in lib 22

10005	2	13	7
10012	0	9	9
10606	0	9	9
11188	1	15	15
11500	25	74	3
11566	25	74	3
11568	12	27	2
11629	5	16	3
11636	5	16	3
11691	12	27	2
11879	0	6	6
12906	0	6	6
13047	13	42	3
13051	13	42	3
13069	263	962	4
13141	0	6	6
13187	0	6	6

5

EXAMPLE 67

POLYNUCLEOTIDES DIFFERENTIALLY EXPRESSED ACROSS MULTIPLE LIBRARIES

A number of polynucleotide sequences have been identified that are differentially expressed between cancerous cells and normal cells across two or more tissue types tested (*i.e.*, breast, colon, lung, and prostate). Expression of these sequences in a tissue of any origin can provide diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant state in these tissues, and can be important in risk assessment for a patient. These polynucleotides can also serve as non-tissue specific markers of, for example, risk of metastasis of a tumor. The following polynucleotides were

10

differentially expressed but without tissue type-specificity in at least two of the breast, colon, lung, and prostate libraries tested: 9972, 10024, 10274, 10331, 10533, 10755, 11361, 11500, 11566, 11568, 11583, 11691, 11701, 11730, 11764, 11775, 11794, 11842, 11979, 11990, 12054, 12065, 12158, 12232, 12297, 12312, 12335, 12379, 12409, 12551, 12593, 12623, 12643, 12668, 12703, 12723, 12878, 12895, 12896, 12899, 12906, 12928, 12966, 13047, 13048, 13051, 13065, 13069, 13075, 13129, 13243, 13250 and 13254.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information:

The following materials were deposited with the American Type Culture Collection (ATCC); CMCC = Chiron Master Culture Collection:

cDNA Libraries Deposited with ATCC

Tube Number	Deposit Date	ATCC Accession No.	CMCC Accession No.
ES137	May 30, 2000		
ES138	May 30, 2000		
ES139	May 30, 2000		
ES140	May 30, 2000		
ES141	May 30, 2000		
ES142	May 30, 2000		
ES143	May 30, 2000		

Tube Number	Deposit Date	ATCC Accession No.	CMCC Accession No.
ES137	May 30, 2000		
ES144	May 30, 2000		
ES145	May 30, 2000		
ES146	May 30, 2000		
ES147	May 30, 2000		
ES148	May 30, 2000		
ES149	May 30, 2000		
ES150	May 30, 2000		
ES151	May 30, 2000		
ES152	May 30, 2000		
ES153	May 30, 2000		
ES154	May 30, 2000		
ES155	May 30, 2000		
ES156	May 30, 2000		
ES157	May 30, 2000		
ES158	May 30, 2000		
ES159	May 30, 2000		
ES160	May 30, 2000		
ES161	May 30, 2000		
ES162	May 30, 2000		
ES163	May 30, 2000		
ES164	May 30, 2000		
ES165	May 30, 2000		
ES166	May 30, 2000		
ES167	May 30, 2000		

Table 105 lists the clones for each deposit, designated as “tube” number. This deposit is provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

10 Retrieval of Individual Clones from Deposit of Pooled Clones

Where the ATCC deposit is composed of a pool of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones were then deposited as a pool of equal mixtures in the composite deposit. Particular clones

can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Table 105

15

Clone Name	Tube
M00001351A:B02	ES 137
M00001356A:H11	ES 137
M00001363D:D09	ES 137
M00001395D:H02	ES 137
M00001439C:H06	ES 137
M00001476B:G10	ES 137
M00001582A:E02	ES 137
M00003750D:E06	ES 137
M00003761C:F02	ES 137
M00003770A:E05	ES 137
M00003786A:A11	ES 137
M00003800A:F09	ES 137
M00003816D:E11	ES 137
M00003902A:C03	ES 137
M00003991C:F06	ES 137
M00003995B:E03	ES 137
M00004046C:A08	ES 137
M00004105D:D05	ES 137
M00004139B:B10	ES 137
M00004140D:C03	ES 137
M00004144A:H05	ES 137
M00004152A:C12	ES 137
M00004155D:A10	ES 137
M00004168A:G11	ES 137
M00004197B:H10	ES 137
M00004222C:E03	ES 137
M00004234A:E07	ES 137
M00004239B:F11	ES 137
M00004241B:H07	ES 137
M00004264B:A05	ES 137
M00004278A:F09	ES 137
M00004282D:C11	ES 137
M00004308C:C06	ES 137
M00004340C:C07	ES 137
M00004354D:E05	ES 137
M00004361A:H02	ES 137
M00004372B:F07	ES 137
M00004378A:B10	ES 137
M00004393B:E07	ES 137
M00023282A:C02	ES 137
M00023300D:C11	ES 137
M00023316C:G08	ES 137
M00023333D:C12	ES 137
M00023352B:F03	ES 137
M00023352D:H03	ES 137
M00023376B:G04	ES 137
M00023377B:F01	ES 137
M00023398B:D12	ES 137
M00023399C:E10	ES 137

Clone Name	Tube
M00026803A:F08	ES 137
M00026843B:D10	ES 137
M00026850D:F09	ES 137
M00026851B:F01	ES 137
M00026856D:F02	ES 137
M00026857D:G12	ES 137
M00026859D:D01	ES 137
M00026860B:C05	ES 137
M00026865B:A06	ES 137
M00026868C:E11	ES 137
M00026878A:F05	ES 137
M00026882D:G09	ES 137
M00026885A:H09	ES 137
M00026901A:G07	ES 137
M00026914A:H10	ES 137
M00026915B:C06	ES 137
M00026918B:D01	ES 137
M00026922C:B02	ES 137
M00026922C:G03	ES 137
M00026926A:E10	ES 137
M00026927D:F02	ES 137
M00026928D:A03	ES 137
M00026935C:B04	ES 137
M00026941D:A04	ES 137
M00026944B:E03	ES 137
M00026946A:F12	ES 137
M00026980A:D09	ES 137
M00027016A:B06	ES 137
M00027018A:C09	ES 137
M00027021A:G02	ES 137
M00027022D:G11	ES 137
M00027030C:H06	ES 137
M00027035D:C06	ES 137
M00027049B:F05	ES 137
M00027078A:B02	ES 137
M00027080A:B01	ES 137
M00027085C:E11	ES 137
M00027094A:B03	ES 137
M00027103B:A09	ES 137
M00027108C:B03	ES 137
M00027121D:C05	ES 137
M00027135A:B11	ES 137
M00027136C:C09	ES 137
M00027141C:H03	ES 137
M00027159D:F03	ES 137
M00027162B:F05	ES 137
M00027178B:G09	ES 137
M00027179D:E06	ES 138
M00027181D:A05	ES 138

Clone Name	Tube
M00027195C:E04	ES 138
M00027198B:B08	ES 138
M00027200A:F02	ES 138
M00027207B:F07	ES 138
M00027212D:E03	ES 138
M00027228D:A01	ES 138
M00027232D:B08	ES 138
M00027233B:C01	ES 138
M00027236A:E04	ES 138
M00027237C:B08	ES 138
M00027248A:C02	ES 138
M00027256B:H09	ES 138
M00027258A:A07	ES 138
M00027263A:F10	ES 138
M00027292D:F10	ES 138
M00027297A:C04	ES 138
M00027299B:B12	ES 138
M00027301A:G05	ES 138
M00027301B:B08	ES 138
M00027314C:D09	ES 138
M00027319D:B11	ES 138
M00027324D:C05	ES 138
M00027347C:G07	ES 138
M00027355A:B07	ES 138
M00027359B:G05	ES 138
M00027366A:F11	ES 138
M00027379C:B07	ES 138
M00027392B:H02	ES 138
M00027396D:G08	ES 138
M00027398C:F07	ES 138
M00027438C:G07	ES 138
M00027462A:D07	ES 138
M00027462B:H07	ES 138
M00027468A:C09	ES 138
M00027475B:E10	ES 138
M00027476A:C09	ES 138
M00027486A:F06	ES 138
M00027520A:C05	ES 138
M00027525B:D06	ES 138
M00027526D:F03	ES 138
M00027528C:B10	ES 138
M00027537C:B01	ES 138
M00027546C:B10	ES 138
M00027591B:C04	ES 138
M00027596A:A10	ES 138
M00027596C:E06	ES 138
M00027602B:C01	ES 138
M00027615A:F10	ES 138
M00027617B:C12	ES 138

Clone Name	Tube
M00027620D:F11	ES 138
M00027625A:H01	ES 138
M00027634A:D11	ES 138
M00027641C:A03	ES 138
M00027647C:D03	ES 138
M00027652B:F11	ES 138
M00027668C:H12	ES 138
M00027729D:H06	ES 138
M00027733A:A02	ES 138
M00027741B:F09	ES 138
M00027743A:C03	ES 138
M00027801C:C11	ES 138
M00027813C:F01	ES 138
M00027818C:C07	ES 138
M00027836D:F12	ES 138
M00027837C:D09	ES 138
M00028120D:F12	ES 138
M00028066C:D07	ES 138
M00028184D:G10	ES 138
M00028185B:A06	ES 138
M00028196D:A03	ES 138
M00028201B:H12	ES 138
M00028207D:E09	ES 138
M00028210B:D02	ES 138
M00028212C:B08	ES 138
M00028215D:F03	ES 138
M00028220A:B04	ES 138
M00028314D:F05	ES 138
M00028316B:H12	ES 138
M00028354A:B12	ES 138
M00028354D:A03	ES 138
M00028357A:G10	ES 138
M00028362A:G11	ES 138
M00028364C:G08	ES 138
M00028369D:E08	ES 138
M00028617C:A12	ES 138
M00028768C:D05	ES 138
M00028770A:D04	ES 138
M00028772C:B09	ES 138
M00028775D:F03	ES 138
M00028777B:G12	ES 138
M00031368A:E10	ES 138
M00031417C:G09	ES 138
M00031419D:C04	ES 138
M00031485D:G02	ES 138
M00032480B:E10	ES 139
M00032492A:C01	ES 139
M00032495B:D02	ES 139
M00032499C:A01	ES 139

Clone Name	Tube
M00032508B:H03	ES 139
M00032510D:F12	ES 139
M00032510D:G06	ES 139
M00032513D:F01	ES 139
M00032530D:C02	ES 139
M00032535D:H01	ES 139
M00032539B:C11	ES 139
M00032540A:A09	ES 139
M00032541D:H08	ES 139
M00032545B:H09	ES 139
M00032545D:G05	ES 139
M00032550D:C02	ES 139
M00032551B:G05	ES 139
M00032577A:C04	ES 139
M00032578A:G06	ES 139
M00032584A:H08	ES 139
M00032592A:H11	ES 139
M00032597C:B01	ES 139
M00032638C:G08	ES 139
M00032638D:A06	ES 139
M00032668D:G12	ES 139
M00032678C:D06	ES 139
M00032688D:D11	ES 139
M00032712B:G02	ES 139
M00032724A:C05	ES 139
M00032725C:F06	ES 139
M00032726C:C01	ES 139
M00032731B:C10	ES 139
M00032731C:C07	ES 139
M00032737B:E09	ES 139
M00032739A:A06	ES 139
M00032744B:F10	ES 139
M00032766B:D12	ES 139
M00032766C:A04	ES 139
M00032790B:A07	ES 139
M00032793A:F06	ES 139
M00032797B:G02	ES 139
M00032808B:G10	ES 139
M00032811B:D02	ES 139
M00032829B:E06	ES 139
M00032830D:G03	ES 139
M00032831C:G07	ES 139
M00032853D:G12	ES 139
M00032864B:B09	ES 139
M00032871D:E11	ES 139
M00032876C:D06	ES 139
M00032907A:G04	ES 139
M00032909A:B06	ES 139
M00032917D:G09	ES 139

Clone Name	Tube
M00032918B:D08	ES 139
M00032918B:E06	ES 139
M00032918C:B10	ES 139
M00032921B:H08	ES 139
M00032933A:C10	ES 139
M00032939B:E07	ES 139
M00032940A:C02	ES 139
M00032942D:C12	ES 139
M00032944B:B02	ES 139
M00032984C:G05	ES 139
M00032990B:A11	ES 139
M00032994A:A08	ES 139
M00032995C:C05	ES 139
M00033007C:E01	ES 139
M00033019B:E10	ES 139
M00033033C:H01	ES 139
M00033034C:A06	ES 139
M00033034C:F02	ES 139
M00033037D:C11	ES 139
M00033074A:C08	ES 139
M00033130B:F06	ES 139
M00033140D:F06	ES 139
M00033173D:C01	ES 139
M00033176B:E12	ES 139
M00033186C:D11	ES 139
M00033189D:F08	ES 139
M00033202D:G06	ES 139
M00033204B:A07	ES 139
M00033205A:F03	ES 139
M00033217B:H07	ES 139
M00033218A:C04	ES 139
M00033223B:H07	ES 139
M00033226A:A11	ES 139
M00033231D:B09	ES 139
M00033231D:G10	ES 139
M00033243B:A05	ES 139
M00033246C:E08	ES 139
M00033248A:B02	ES 139
M00033261C:D12	ES 139
M00033262D:A11	ES 139
M00033263B:G04	ES 139
M00033276B:G08	ES 139
M00033185C:D01	ES 139
M00033288B:D12	ES 140
M00033300D:H12	ES 140
M00033306D:G08	ES 140
M00033306D:H09	ES 140
M00033308B:G05	ES 140
M00033343C:H08	ES 140

Clone Name	Tube
M00033345D:A09	ES 140
M00033346C:A05	ES 140
M00033347C:F02	ES 140
M00033349D:F05	ES 140
M00033358A:H12	ES 140
M00033362C:C05	ES 140
M00033375A:G04	ES 140
M00033376A:C12	ES 140
M00033377D:A05	ES 140
M00033410B:C09	ES 140
M00033424B:A04	ES 140
M00033424D:H12	ES 140
M00033425A:C10	ES 140
M00033427D:F01	ES 140
M00033432B:H10	ES 140
M00033437C:A07	ES 140
M00033437C:C03	ES 140
M00033442A:D06	ES 140
M00033446C:G08	ES 140
M00033446D:B02	ES 140
M00033450C:A02	ES 140
M00033451A:H01	ES 140
M00033454A:D09	ES 140
M00033457D:A05	ES 140
M00033560D:G07	ES 140
M00033561C:A02	ES 140
M00033566C:E08	ES 140
M00033570B:C08	ES 140
M00033570B:E06	ES 140
M00033570C:C10	ES 140
M00033578D:G02	ES 140
M00033581C:H10	ES 140
M00033581D:D08	ES 140
M00033583B:E06	ES 140
M00033583D:B05	ES 140
M00033584D:G11	ES 140
M00033585D:A02	ES 140
M00033588C:G04	ES 140
M00033594C:B03	ES 140
M00033595A:C11	ES 140
M00038259A:G08	ES 140
M00038259B:A02	ES 140
M00038259B:G08	ES 140
M00038259C:H09	ES 140
M00038272A:G01	ES 140
M00038272D:F11	ES 140
M00038279C:A11	ES 140
M00038284B:H04	ES 140
M00038303A:C03	ES 140

Clone Name	Tube
M00038303C:D02	ES 140
M00038303D:E07	ES 140
M00038315C:G11	ES 140
M00038325D:F12	ES 140
M00038326B:D04	ES 140
M00038327A:C11	ES 140
M00038327D:A05	ES 140
M00038328D:A03	ES 140
M00038329A:E08	ES 140
M00038387B:A07	ES 140
M00038614C:H11	ES 140
M00038615A:H12	ES 140
M00038616D:B12	ES 140
M00038618C:C08	ES 140
M00038619B:A03	ES 140
M00038620B:E09	ES 140
M00038631C:B10	ES 140
M00038631D:B02	ES 140
M00038632C:B09	ES 140
M00038633A:D07	ES 140
M00038633B:G02	ES 140
M00038635A:G09	ES 140
M00038635B:C08	ES 140
M00038638D:H03	ES 140
M00038639B:C03	ES 140
M00038639D:F07	ES 140
M00038661A:A07	ES 140
M00038662B:A12	ES 140
M00038663B:H06	ES 140
M00038663D:H10	ES 140
M00038664C:E04	ES 140
M00038991A:D01	ES 140
M00038994A:A10	ES 140
M00038995C:G08	ES 140
M00038995D:E05	ES 140
M00038999B:G11	ES 140
M00038999D:C11	ES 140
M00039002D:G11	ES 140
M00039004B:A06	ES 140
M00039004B:C11	ES 140
M00039005C:H01	ES 141
M00039006D:B01	ES 141
M00039011D:C10	ES 141
M00039013A:C09	ES 141
M00039013D:F02	ES 141
M00039014A:H10	ES 141
M00039014B:C04	ES 141
M00039015A:D07	ES 141
M00039015B:G10	ES 141

Clone Name	Tube
M00039015B:H09	ES 141
M00039015D:H04	ES 141
M00039016A:A02	ES 141
M00039016D:G06	ES 141
M00039024B:B10	ES 141
M00039025A:H09	ES 141
M00039026D:F05	ES 141
M00039028C:B11	ES 141
M00039030B:E02	ES 141
M00039036C:B05	ES 141
M00039039B:E03	ES 141
M00039039B:F09	ES 141
M00039042B:B02	ES 141
M00039043B:E01	ES 141
M00039049D:G07	ES 141
M00039050A:H10	ES 141
M00039052C:F07	ES 141
M00039058A:A04	ES 141
M00039058C:H02	ES 141
M00039059C:G08	ES 141
M00039061B:F08	ES 141
M00039063B:D08	ES 141
M00039064D:H09	ES 141
M00039066D:G08	ES 141
M00039068B:B04	ES 141
M00039068C:E06	ES 141
M00039070D:C02	ES 141
M00039072C:C03	ES 141
M00039072C:E02	ES 141
M00039079A:A05	ES 141
M00039080C:H06	ES 141
M00039081B:G06	ES 141
M00039082B:A05	ES 141
M00039084C:G07	ES 141
M00039084C:H03	ES 141
M00039084C:H04	ES 141
M00039084D:D07	ES 141
M00039096A:A05	ES 141
M00039096A:E07	ES 141
M00039097D:D06	ES 141
M00039099A:H08	ES 141
M00039104D:C09	ES 141
M00039105C:B08	ES 141
M00039107C:E04	ES 141
M00039108D:B06	ES 141
M00039112B:C05	ES 141
M00039118B:C05	ES 141
M00039118D:A06	ES 141
M00039120C:C09	ES 141

Clone Name	Tube
M00039120C:H03	ES 141
M00039123A:B10	ES 141
M00039124C:F03	ES 141
M00039124C:H02	ES 141
M00039124C:H08	ES 141
M00039126D:A08	ES 141
M00039127A:G11	ES 141
M00039127D:E10	ES 141
M00039129C:D04	ES 141
M00039133B:F08	ES 141
M00039135D:F05	ES 141
M00039135D:G02	ES 141
M00039135D:H02	ES 141
M00039139A:C09	ES 141
M00039139C:G12	ES 141
M00039140A:B08	ES 141
M00039140D:A04	ES 141
M00039140D:D09	ES 141
M00039141C:E01	ES 141
M00039142D:B11	ES 141
M00039144C:E06	ES 141
M00039147A:F10	ES 141
M00039156A:B11	ES 141
M00039158B:G12	ES 141
M00039166B:G06	ES 141
M00039167B:H09	ES 141
M00039168C:A04	ES 141
M00039169A:E12	ES 141
M00039170A:B10	ES 141
M00039170C:F05	ES 141
M00039171B:D11	ES 141
M00039177B:D03	ES 141
M00039179A:G09	ES 141
M00039180A:A07	ES 141
M00039196B:H06	ES 141
M00039196D:A07	ES 141
M00039200A:C10	ES 141
M00039211A:C12	ES 141
M00039212C:C12	ES 142
M00039213A:D01	ES 142
M00039213B:F05	ES 142
M00039218A:F03	ES 142
M00039221A:H03	ES 142
M00039224A:E12	ES 142
M00039228A:B05	ES 142
M00039230A:A10	ES 142
M00039230D:D09	ES 142
M00039230D:G12	ES 142
M00039233A:A03	ES 142

Clone Name	Tube
M00039238A:B12	ES 142
M00039238D:A08	ES 142
M00039241A:E11	ES 142
M00039249A:C12	ES 142
M00039249C:G11	ES 142
M00039255C:E12	ES 142
M00039257D:C03	ES 142
M00039258B:E06	ES 142
M00039258D:B08	ES 142
M00039260C:G03	ES 142
M00039263D:A12	ES 142
M00039266A:B02	ES 142
M00039266D:F12	ES 142
M00039266D:H04	ES 142
M00039273B:F02	ES 142
M00039273D:B02	ES 142
M00039274B:G07	ES 142
M00039276B:H09	ES 142
M00039277D:G10	ES 142
M00039279B:C11	ES 142
M00039279B:H02	ES 142
M00039279C:B08	ES 142
M00039281D:B04	ES 142
M00039284D:B12	ES 142
M00039286A:C06	ES 142
M00039287C:A06	ES 142
M00039288C:B11	ES 142
M00039293A:H04	ES 142
M00039293B:C11	ES 142
M00039295B:D03	ES 142
M00039297C:H08	ES 142
M00039298B:B06	ES 142
M00039298B:D03	ES 142
M00039298D:B04	ES 142
M00039299B:G12	ES 142
M00039300C:C09	ES 142
M00039300C:G04	ES 142
M00039301B:F06	ES 142
M00039303C:F11	ES 142
M00039304D:B09	ES 142
M00039308B:G08	ES 142
M00039310A:C07	ES 142
M00039313D:G04	ES 142
M00039316A:C01	ES 142
M00039318B:B09	ES 142
M00039319B:H12	ES 142
M00039319C:A04	ES 142
M00039322A:F04	ES 142
M00039328D:D07	ES 142

Clone Name	Tube
M00039329A:C01	ES 142
M00039329C:B10	ES 142
M00039333D:D09	ES 142
M00039334B:E03	ES 142
M00039335A:E08	ES 142
M00039339A:H07	ES 142
M00039339C:F03	ES 142
M00039340A:D05	ES 142
M00039340B:E07	ES 142
M00039340B:G08	ES 142
M00039341C:H11	ES 142
M00039341D:D07	ES 142
M00039343B:F12	ES 142
M00039344B:G07	ES 142
M00039345A:D09	ES 142
M00039345C:C12	ES 142
M00039381C:H08	ES 142
M00039381D:C02	ES 142
M00039384C:E02	ES 142
M00039384C:F08	ES 142
M00039385B:E09	ES 142
M00039391D:F08	ES 142
M00039396D:B04	ES 142
M00039397B:H09	ES 142
M00039398A:B10	ES 142
M00039401B:D02	ES 142
M00039402B:E03	ES 142
M00039403A:G12	ES 142
M00039404B:A05	ES 142
M00039407B:G02	ES 142
M00039411C:E07	ES 142
M00039412D:G06	ES 142
M00039414D:G03	ES 142
M00039415D:E01	ES 142
M00039417A:D03	ES 142
M00039417A:E12	ES 142
M00039417B:F01	ES 143
M00039417C:A01	ES 143
M00039417C:G01	ES 143
M00039418B:D08	ES 143
M00039420D:D03	ES 143
M00039422D:F04	ES 143
M00039425C:G01	ES 143
M00039425D:E12	ES 143
M00039428C:E01	ES 143
M00039430B:F12	ES 143
M00039431B:F04	ES 143
M00039432C:A01	ES 143
M00039444C:H02	ES 143

Clone Name	Tube
M00039452C:G09	ES 143
M00039454B:A11	ES 143
M00039455D:H04	ES 143
M00039456A:C08	ES 143
M00039458B:H11	ES 143
M00039461A:F04	ES 143
M00039465A:A08	ES 143
M00039472C:B08	ES 143
M00039475C:E10	ES 143
M00039476B:A02	ES 143
M00039477A:B03	ES 143
M00039477D:A10	ES 143
M00039611D:D11	ES 143
M00039612B:B10	ES 143
M00039612B:G05	ES 143
M00039616A:B10	ES 143
M00039616B:C01	ES 143
M00039619B:D02	ES 143
M00039631A:C10	ES 143
M00039633D:D05	ES 143
M00039636C:D11	ES 143
M00039637C:A10	ES 143
M00039652B:D05	ES 143
M00039655B:H09	ES 143
M00039655C:C07	ES 143
M00039655C:E08	ES 143
M00039660C:C10	ES 143
M00039663C:G09	ES 143
M00039664D:G07	ES 143
M00039672D:D10	ES 143
M00039673A:F09	ES 143
M00039675D:B03	ES 143
M00039675D:H05	ES 143
M00039677A:B08	ES 143
M00039681B:H09	ES 143
M00039682A:C08	ES 143
M00039682C:H11	ES 143
M00039684D:B08	ES 143
M00039685A:A08	ES 143
M00039686C:C05	ES 143
M00039686C:E06	ES 143
M00039688C:G06	ES 143
M00039689C:E08	ES 143
M00039696A:E05	ES 143
M00039697B:F11	ES 143
M00039700B:D02	ES 143
M00039702A:B12	ES 143
M00039702A:B02	ES 143
M00039705D:F02	ES 143

Clone Name	Tube
M00039707A:D02	ES 143
M00039710C:G03	ES 143
M00039720D:D02	ES 143
M00039727C:B09	ES 143
M00039729A:A10	ES 143
M00039771C:E11	ES 143
M00039773D:A09	ES 143
M00039773D:F11	ES 143
M00039774C:A03	ES 143
M00039774C:C09	ES 143
M00039775A:A09	ES 143
M00039777C:E05	ES 143
M00039778B:G03	ES 143
M00039778C:A04	ES 143
M00039781D:D10	ES 143
M00039782A:H10	ES 143
M00039785D:G05	ES 143
M00039788A:E03	ES 143
M00039788B:A06	ES 143
M00039788C:A01	ES 143
M00039790B:D03	ES 143
M00039792A:B04	ES 143
M00039793D:C05	ES 143
M00039794A:E04	ES 143
M00039795B:H10	ES 143
M00039795D:E10	ES 143
M00039795D:G06	ES 143
M00039797C:G05	ES 143
M00039798B:B02	ES 143
M00039799A:D10	ES 143
M00039801A:H11	ES 143
M00039807A:D01	ES 143
M00039808D:H02	ES 143
M00039810A:H10	ES 143
M00039813B:B01	ES 144
M00039813B:D11	ES 144
M00039815C:F09	ES 144
M00039816B:D04	ES 144
M00039816C:D05	ES 144
M00039820A:F11	ES 144
M00039820A:H11	ES 144
M00039820B:B06	ES 144
M00039827B:F07	ES 144
M00039828B:C05	ES 144
M00039832A:B12	ES 144
M00039835A:F07	ES 144
M00039838A:F05	ES 144
M00039839B:B01	ES 144
M00039839C:E05	ES 144

Clone Name	Tube
M00039847A:F06	ES 144
M00039851B:G11	ES 144
M00039851C:D12	ES 144
M00039854B:F09	ES 144
M00039855C:F01	ES 144
M00039857B:G10	ES 144
M00039859A:F06	ES 144
M00039859C:G10	ES 144
M00039864A:A07	ES 144
M00039866B:A08	ES 144
M00039869B:F06	ES 144
M00039875D:A10	ES 144
M00039876D:H09	ES 144
M00039877C:C03	ES 144
M00039879C:F05	ES 144
M00039879D:B11	ES 144
M00039880A:H11	ES 144
M00039884A:H11	ES 144
M00039885C:D01	ES 144
M00039887C:E07	ES 144
M00039887D:C04	ES 144
M00039888B:D03	ES 144
M00039890A:H05	ES 144
M00039894C:H07	ES 144
M00039896C:H01	ES 144
M00039897D:C10	ES 144
M00039898A:A08	ES 144
M00039898D:C06	ES 144
M00039903A:H07	ES 144
M00039903C:D01	ES 144
M00039903C:F03	ES 144
M00039909C:G05	ES 144
M00039909D:C02	ES 144
M00039910C:G10	ES 144
M00039914D:G12	ES 144
M00039915D:C11	ES 144
M00039927A:F04	ES 144
M00039928B:G05	ES 144
M00039936C:C05	ES 144
M00039938C:A08	ES 144
M00039938C:E11	ES 144
M00039940A:D07	ES 144
M00039940D:G08	ES 144
M00039973D:C08	ES 144
M00039973D:D12	ES 144
M00039975C:C11	ES 144
M00039976D:A12	ES 144
M00039978A:G03	ES 144
M00039981A:E08	ES 144

Clone Name	Tube
M00039982C:H04	ES 144
M00039983D:A06	ES 144
M00039984A:C02	ES 144
M00039984B:G12	ES 144
M00039984D:G12	ES 144
M00039987A:F09	ES 144
M00039987C:E12	ES 144
M00039987C:G08	ES 144
M00039988A:E06	ES 144
M00039990C:D10	ES 144
M00040004D:B03	ES 144
M00040005B:C11	ES 144
M00040005D:B07	ES 144
M00040007D:A06	ES 144
M00040009D:B07	ES 144
M00040010A:F10	ES 144
M00040014B:D01	ES 144
M00040014D:D10	ES 144
M00040014D:F03	ES 144
M00040015C:F08	ES 144
M00040016C:H12	ES 144
M00040017A:C06	ES 144
M00040017D:G03	ES 144
M00040019A:E01	ES 144
M00040021A:F09	ES 144
M00040022C:D06	ES 144
M00040026B:F06	ES 144
M00040029A:B03	ES 144
M00040029A:G04	ES 144
M00040031A:E06	ES 144
M00040032A:B03	ES 144
M00040032A:D09	ES 144
M00040037A:E11	ES 145
M00040038D:G04	ES 145
M00040039D:D06	ES 145
M00040040A:A06	ES 145
M00040041C:C09	ES 145
M00040042B:A10	ES 145
M00040047C:F05	ES 145
M00040052D:F12	ES 145
M00040055D:A06	ES 145
M00040055D:B01	ES 145
M00040060C:H10	ES 145
M00040062B:B05	ES 145
M00040070B:B07	ES 145
M00040071B:A10	ES 145
M00040072C:G09	ES 145
M00040076C:D06	ES 145
M00040077D:C11	ES 145

Clone Name	Tube
M00040080C:C06	ES 145
M00040081C:E01	ES 145
M00040085D:A10	ES 145
M00040085D:E04	ES 145
M00040087D:F08	ES 145
M00040088C:E10	ES 145
M00040089A:G08	ES 145
M00040089B:E04	ES 145
M00040089C:E06	ES 145
M00040090B:G09	ES 145
M00040092B:F05	ES 145
M00040093B:C02	ES 145
M00040093D:D03	ES 145
M00040097A:C12	ES 145
M00040098C:B01	ES 145
M00040098D:E04	ES 145
M00040098D:G12	ES 145
M00040100C:E05	ES 145
M00040100D:B06	ES 145
M00040103B:H10	ES 145
M00040105C:F11	ES 145
M00040106B:B09	ES 145
M00040107B:H07	ES 145
M00040111C:D05	ES 145
M00040115B:A04	ES 145
M00040115B:H12	ES 145
M00040118D:G10	ES 145
M00040121B:C05	ES 145
M00040122D:A02	ES 145
M00040123A:A09	ES 145
M00040124D:H01	ES 145
M00040129D:E10	ES 145
M00040302C:A04	ES 145
M00040304B:F06	ES 145
M00040305A:D11	ES 145
M00040305C:H06	ES 145
M00040307B:F01	ES 145
M00040307C:F10	ES 145
M00040309A:E11	ES 145
M00004825D:D05	ES 145
M00004832D:H02	ES 145
M00004839C:H02	ES 145
M00005018A:B05	ES 145
M00005297D:H08	ES 145
M00005308A:D06	ES 145
M00005351C:G05	ES 145
M00005352C:A02	ES 145
M00005358B:B06	ES 145
M00005359A:D04	ES 145

Clone.Name	Tube
M00005379A:E04	ES 145
M00005382B:F08	ES 145
M00005384A:C11	ES 145
M00005402B:F08	ES 145
M00005445D:B01	ES 145
M00005449B:B10	ES 145
M00005449B:D01	ES 145
M00005457C:A03	ES 145
M00005458A:F11	ES 145
M00005498A:H06	ES 145
M00005531D:F06	ES 145
M00005539D:G01	ES 145
M00005555A:A10	ES 145
M00005556B:D02	ES 145
M00005601D:D08	ES 145
M00005614B:B01	ES 145
M00005623A:G02	ES 145
M00005623D:G12	ES 145
M00005625A:C02	ES 145
M00005673B:B12	ES 145
M00005778B:F09	ES 145
M00005805D:D12	ES 145
M00005820C:E04	ES 145
M00006581D:F08	ES 145
M00006599D:B02	ES 145
M00006657C:G05	ES 145
M00006680B:D02	ES 145
M00006712C:H09	ES 145
M00006809B:B09	ES 145
M00006861B:F09	ES 145
M00006866A:D07	ES 146
M00006886D:H02	ES 146
M00006893C:E07	ES 146
M00006897A:H02	ES 146
M00006928D:D07	ES 146
M00006935C:F06	ES 146
M00006968A:G08	ES 146
M00006977C:G04	ES 146
M00006977D:A03	ES 146
M00007012D:H08	ES 146
M00007013A:D09	ES 146
M00007026B:H09	ES 146
M00007108B:A02	ES 146
M00007112C:B10	ES 146
M00007116C:G02	ES 146
M00007124D:H10	ES 146
M00007136A:A03	ES 146

Clone Name	Tube
M00007149A:G02	ES 146
M00007157C:F11	ES 146
M00007165B:G11	ES 146
M00007194A:B09	ES 146
M00007929C:B08	ES 146
M00007941D:C09	ES 146
M00007943D:C09	ES 146
M00007972B:H12	ES 146
M00007976A:C10	ES 146
M00007992C:F06	ES 146
M00007994A:G02	ES 146
M00008006B:B03	ES 146
M00008026B:C11	ES 146
M00008045A:H02	ES 146
M00008053A:F10	ES 146
M00008063B:A06	ES 146
M00021665B:F12	ES 146
M00021671D:F12	ES 146
M00021852D:A05	ES 146
M00021866D:A03	ES 146
M00021908D:G12	ES 146
M00021919C:A10	ES 146
M00021923C:D11	ES 146
M00021955A:H02	ES 146
M00021964C:E10	ES 146
M00021972D:C11	ES 146
M00022005C:C06	ES 146
M00022015B:B07	ES 146
M00022054A:H03	ES 146
M00022084D:B01	ES 146
M00022099B:D06	ES 146
M00022105C:C12	ES 146
M00022127C:H03	ES 146
M00022135C:B05	ES 146
M00022138A:E05	ES 146
M00022175D:D12	ES 146
M00022178B:D06	ES 146
M00022181C:D01	ES 146
M00022183B:C02	ES 146
M00022184C:C11	ES 146
M00022233C:A12	ES 146
M00022234C:D06	ES 146
M00022247A:E02	ES 146
M00022257A:B09	ES 146
M00022262D:G03	ES 146

Clone Name	Tube
M00022264B:G10	ES 146
M00022363C:G12	ES 146
M00022365D:A03	ES 146
M00022373A:B05	ES 146
M00022373C:B07	ES 146
M00022391B:E01	ES 146
M00022391D:F10	ES 146
M00022416A:A07	ES 146
M00022421B:C11	ES 146
M00022433A:E02	ES 146
M00022434D:D06	ES 146
M00022440B:E01	ES 146
M00022444D:G01	ES 146
M00022467C:B12	ES 146
M00022489C:G04	ES 146
M00022492C:A02	ES 146
M00022495D:H08	ES 146
M00022496B:E12	ES 146
M00022499A:B02	ES 146
M00022533A:A08	ES 146
M00022579C:C11	ES 146
M00022597D:A06	ES 146
M00022602A:E09	ES 146
M00022615D:G05	ES 146
M00022634D:C08	ES 146
M00022640C:C12	ES 146
M00022641C:H05	ES 146
M00022646A:H10	ES 146
M00022662D:G11	ES 146
M00022667D:B02	ES 146
M00022668B:B12	ES 146
M00022670D:H11	ES 146
M00022671B:A08	ES 146
M00022684A:C02	ES 146
M00022731A:D02	ES 147
M00022739A:B03	ES 147
M00022747D:E03	ES 147
M00022767B:G11	ES 147
M00022785C:G06	ES 147
M00022793D:B01	ES 147
M00022795B:G06	ES 147
M00022797B:G08	ES 147
M00022817A:H02	ES 147
M00022821C:C09	ES 147
M00022823C:C01	ES 147

Clone Name	Tube
M00022830D:D01	ES 147
M00022834B:G11	ES 147
M00022854A:B03	ES 147
M00022856C:A07	ES 147
M00022860C:G04	ES 147
M00022885C:H05	ES 147
M00022895A:H08	ES 147
M00022910A:A06	ES 147
M00022925C:A08	ES 147
M00022928B:C01	ES 147
M00022930C:E02	ES 147
M00022938B:F07	ES 147
M00022968B:E02	ES 147
M00022976C:F04	ES 147
M00022979A:D05	ES 147
M00022986D:H09	ES 147
M00022997A:F06	ES 147
M00023001C:C08	ES 147
M00023003C:D07	ES 147
M00023007A:H04	ES 147
M00023007C:E10	ES 147
M00023020C:G08	ES 147
M00023024D:F12	ES 147
M00023032A:B05	ES 147
M00023039D:B05	ES 147
M00023042D:D02	ES 147
M00023044B:D02	ES 147
M00023094A:B11	ES 147
M00023100A:E12	ES 147
M00039181D:E05	ES 147
M00039184A:D03	ES 147
M00039184B:B09	ES 147
M00039361B:E01	ES 147
M00039363A:C09	ES 147
M00039366C:B07	ES 147
M00039367B:H02	ES 147
M00039371B:H06	ES 147
M00039372C:D12	ES 147
M00039374B:B07	ES 147
M00039374C:H12	ES 147
M00039374C:H02	ES 147
M00039376D:H07	ES 147
M00039377D:E12	ES 147
M00039378D:H07	ES 147
M00039379A:B03	ES 147

Clone Name	Tube
M00039380C:C09	ES 147
M00039482B:G02	ES 147
M00039493A:C04	ES 147
M00039496B:D08	ES 147
M00039496B:H09	ES 147
M00039497C:C06	ES 147
M00039499C:A04	ES 147
M00039500C:C04	ES 147
M00039505C:E03	ES 147
M00039508A:C12	ES 147
M00039508C:G01	ES 147
M00039510C:G02	ES 147
M00039512C:D06	ES 147
M00039515A:A06	ES 147
M00039515D:C11	ES 147
M00039517B:G12	ES 147
M00039521A:A02	ES 147
M00039521D:H03	ES 147
M00039528B:B12	ES 147
M00039529C:D07	ES 147
M00039530B:E02	ES 147
M00039533A:C12	ES 147
M00039533B:G08	ES 147
M00039533D:F04	ES 147
M00039535D:D10	ES 147
M00039536C:C10	ES 147
M00039536C:H11	ES 147
M00039561A:B07	ES 147
M00039561B:A09	ES 147
M00039562B:G02	ES 147
M00039564B:C01	ES 147
M00039570A:D10	ES 147
M00039570B:D10	ES 147
M00039584C:C01	ES 147
M00039584C:C11	ES 147
M00039587C:F12	ES 147
M00039590D:D02	ES 147
M00039591C:D06	ES 147
M00039595C:E05	ES 147
M00039597D:F04	ES 147
M00039600A:A11	ES 148
M00039604B:E05	ES 148
M00039604D:G03	ES 148
M00039606B:D08	ES 148
M00039607D:E08	ES 148

Clone Name	Tube
M00039608D:H01	ES 148
M00039609D:F07	ES 148
M00039624A:H09	ES 148
M00039624B:F12	ES 148
M00039625B:G08	ES 148
M00039626D:F04	ES 148
M00039629B:F01	ES 148
M00039629D:B04	ES 148
M00039630A:C08	ES 148
M00039630C:H04	ES 148
M00039641A:A05	ES 148
M00039641C:D07	ES 148
M00039642D:B12	ES 148
M00039642D:H09	ES 148
M00039643C:B04	ES 148
M00039645C:E01	ES 148
M00039647A:H11	ES 148
M00039736D:G08	ES 148
M00039740B:F10	ES 148
M00039752B:G08	ES 148
M00039755A:B08	ES 148
M00039756B:H06	ES 148
M00039760B:B08	ES 148
M00040131B:D11	ES 148
M00040131C:F03	ES 148
M00040131D:G08	ES 148
M00040133B:B03	ES 148
M00040136C:F08	ES 148
M00040138B:H03	ES 148
M00040141D:F05	ES 148
M00040143A:H05	ES 148
M00040145D:D03	ES 148
M00040147D:H11	ES 148
M00040160B:A10	ES 148
M00040162A:E01	ES 148
M00040169B:F08	ES 148
M00040173D:B05	ES 148
M00040174C:E10	ES 148
M00040174D:G03	ES 148
M00040181B:H09	ES 148
M00040181D:H10	ES 148
M00040182D:D06	ES 148
M00040183A:F07	ES 148
M00040184C:A11	ES 148
M00040191A:B09	ES 148

Clone Name	Tube
M00040221A:G11	ES 148
M00040222D:G02	ES 148
M00040223A:C05	ES 148
M00040226A:H10	ES 148
M00040230A:H02	ES 148
M00040231B:C08	ES 148
M00040232D:B07	ES 148
M00040233A:H02	ES 148
M00040233C:G05	ES 148
M00040252C:C06	ES 148
M00040253C:A05	ES 148
M00040254B:C10	ES 148
M00040256A:A06	ES 148
M00040257D:H10	ES 148
M00040260B:D02	ES 148
M00040260C:D04	ES 148
M00040261C:F01	ES 148
M00040262B:B06	ES 148
M00040264D:G05	ES 148
M00040265D:B07	ES 148
M00040265D:C08	ES 148
M00040267A:E06	ES 148
M00040267C:C04	ES 148
M00040271B:E12	ES 148
M00040271C:D08	ES 148
M00040273B:H12	ES 148
M00040274A:D07	ES 148
M00040274A:H11	ES 148
M00040280C:H05	ES 148
M00040281D:B01	ES 148
M00040282A:A03	ES 148
M00040286C:C02	ES 148
M00040287C:B09	ES 148
M00040287D:D07	ES 148
M00039746C:A08	ES 148
M00039746C:G09	ES 148
M00039746C:H05	ES 148
M00039746C:H06	ES 148
M00039746D:D11	ES 148
M00039748A:F11	ES 148
M00039748C:F11	ES 148
M00039749D:D05	ES 148
M00039761D:E10	ES 148
M00039762B:F07	ES 148
M00039764C:D07	ES 148

Clone Name	Tube
M00039766A:G07	ES 148
M00039766D:H01	ES 149
M00039767B:A04	ES 149
M00039767C:E12	ES 149
M00039770A:G11	ES 149
M00039770C:E04	ES 149
M00039942D:C01	ES 149
M00039943B:F10	ES 149
M00039945C:F09	ES 149
M00039946B:F08	ES 149
M00039947A:D06	ES 149
M00039947C:G03	ES 149
M00039948A:E03	ES 149
M00039948D:D11	ES 149
M00039951A:B07	ES 149
M00039951B:B12	ES 149
M00039951B:C03	ES 149
M00039955C:C04	ES 149
M00039957C:C09	ES 149
M00039957D:A12	ES 149
M00039958A:A08	ES 149
M00039958C:B09	ES 149
M00040201C:G11	ES 149
M00040202A:F05	ES 149
M00040203A:H06	ES 149
M00040203B:A05	ES 149
M00040203D:H11	ES 149
M00040206A:A07	ES 149
M00040207B:D08	ES 149
M00040208A:C03	ES 149
M00040208B:A07	ES 149
M00040208D:G09	ES 149
M00040217D:B07	ES 149
M00040218C:C02	ES 149
M00040219B:D02	ES 149
M00040219D:E08	ES 149
M00040291D:C05	ES 149
M00040293D:G04	ES 149
M00040294D:D12	ES 149
M00040296D:E09	ES 149
M00040298B:G02	ES 149
M00040299B:F10	ES 149
M00040313C:D05	ES 149
M00040313D:E04	ES 149
M00040314D:H05	ES 149

Clone Name	Tube
M00040317A:H03	ES 149
M00040317D:F02	ES 149
M00040318A:B02	ES 149
M00040318C:H11	ES 149
M00040320D:F02	ES 149
M00040323B:C12	ES 149
M00040323C:G11	ES 149
M00040326A:F04	ES 149
M00040327B:G06	ES 149
M00040332D:B05	ES 149
M00040333D:G05	ES 149
M00040334D:B02	ES 149
M00040334D:C07	ES 149
M00040342B:D12	ES 149
M00040345D:A09	ES 149
M00040346A:C11	ES 149
M00040347D:F09	ES 149
M00040349D:B09	ES 149
M00040351B:F02	ES 149
M00040351D:A11	ES 149
M00040364A:E05	ES 149
M00040366A:B01	ES 149
M00040368A:A12	ES 149
M00040368A:F01	ES 149
M00040368D:E09	ES 149
M00040371C:H05	ES 149
M00040375C:B06	ES 149
M00040376C:G02	ES 149
M00040377C:G07	ES 149
M00040383A:H02	ES 149
M00040383D:C04	ES 149
M00040385C:D02	ES 149
M00040386A:A02	ES 149
M00040387C:E07	ES 149
M00040387D:H05	ES 149
M00040390A:H02	ES 149
M00040390B:F02	ES 149
M00040391A:D10	ES 149
M00040392B:H01	ES 149
M00040392C:B12	ES 149
M00040394A:D04	ES 149
M00040395B:D11	ES 149
M00042534A:A05	ES 149
M00042538B:E06	ES 149
M00042543C:G04	ES 149

Clone Name	Tube
M00042558A:F03	ES 149
M00042560A:F12	ES 149
M00042565C:A08	ES 149
M00042566C:C05	ES 149
M00042567B:H10	ES 149
M00042693D:E04	ES 149
M00042696B:E05	ES 149
M00042697D:C07	ES 150
M00042698D:D10	ES 150
M00042698D:E01	ES 150
M00042702B:G02	ES 150
M00042704A:F09	ES 150
M00042711B:A11	ES 150
M00042717A:C07	ES 150
M00042737C:H04	ES 150
M00042740A:E09	ES 150
M00042742D:D05	ES 150
M00042887C:D07	ES 150
M00042895A:D10	ES 150
M00042895C:G01	ES 150
M00042902D:B08	ES 150
M00042904B:E07	ES 150
M00042905A:F11	ES 150
M00042905B:C03	ES 150
M00042905D:D02	ES 150
M00042347D:H11	ES 150
M00042348B:E05	ES 150
M00042349D:D07	ES 150
M00042431B:G08	ES 150
M00042431C:F01	ES 150
M00042431D:C10	ES 150
M00042432D:E02	ES 150
M00042435A:A11	ES 150
M00042436B:H09	ES 150
M00042437A:D04	ES 150
M00042439B:B03	ES 150
M00042439B:D03	ES 150
M00042440B:E09	ES 150
M00042463A:F09	ES 150
M00042470C:E05	ES 150
M00042511A:H04	ES 150
M00042515C:F08	ES 150
M00042751C:C12	ES 150
M00042752A:E11	ES 150
M00042756B:F11	ES 150

Clone Name	Tube
M00042756D:A10	ES 150
M00042759B:G11	ES 150
M00042760A:C12	ES 150
M00042765C:D04	ES 150
M00042767B:G10	ES 150
M00042769C:E09	ES 150
M00042770B:B12	ES 150
M00042770C:C04	ES 150
M00042771C:F06	ES 150
M00042774C:C05	ES 150
M00042781A:A07	ES 150
M00042784A:H06	ES 150
M00042788C:F11	ES 150
M00042790C:C07	ES 150
M00042792A:H01	ES 150
M00042797D:D10	ES 150
M00042799D:F08	ES 150
M00042800A:A03	ES 150
M00042802C:C04	ES 150
M00042806C:F07	ES 150
M00042807D:D05	ES 150
M00042823C:C02	ES 150
M00042830B:E02	ES 150
M00042839B:B11	ES 150
M00042841D:H07	ES 150
M00042849D:F11	ES 150
M00042852B:A03	ES 150
M00042852C:A01	ES 150
M00042856B:H02	ES 150
M00042352C:H03	ES 150
M00042352D:C01	ES 150
M00042352D:G09	ES 150
M00042448A:C09	ES 150
M00042448C:H12	ES 150
M00042453B:G09	ES 150
M00042518D:A06	ES 150
M00042518D:D04	ES 150
M00043296B:G09	ES 150
M00043304B:D05	ES 150
M00043304C:D02	ES 150
M00043305B:G02	ES 150
M00043306C:B03	ES 150
M00043306D:B07	ES 150
M00043310C:G06	ES 150
M00043311C:E03	ES 150

Clone Name	Tube
M00043312C:E08	ES 150
M00043320B:A07	ES 150
M00043324D:H11	ES 150
M00043328D:H02	ES 150
M00043332C:G04	ES 150
M00043334B:A10	ES 150
M00043338B:A03	ES 150
M00043338B:C11	ES 150
M00043339A:F11	ES 150
M00043340B:H08	ES 150
M00043344D:E04	ES 150
M00043345C:A06	ES 150
M00043346A:G01	ES 150
M00043350D:B11	ES 151
M00043351D:A11	ES 151
M00043352D:B05	ES 151
M00043352D:C03	ES 151
M00043359B:D10	ES 151
M00043359C:G01	ES 151
M00043361B:A01	ES 151
M00043366A:A02	ES 151
M00043366C:H05	ES 151
M00043367B:A08	ES 151
M00043368C:F09	ES 151
M00043370B:C08	ES 151
M00043372C:G05	ES 151
M00043377A:C03	ES 151
M00043378A:H10	ES 151
M00043379D:H02	ES 151
M00043383C:F12	ES 151
M00043383D:A02	ES 151
M00043384B:B02	ES 151
M00043386A:B08	ES 151
M00043389C:E03	ES 151
M00043389D:D07	ES 151
M00043391A:C10	ES 151
M00043391A:G08	ES 151
M00043392D:C11	ES 151
M00043393A:B08	ES 151
M00043401D:G08	ES 151
M00043402C:D08	ES 151
M00043405A:D11	ES 151
M00043405C:G12	ES 151
M00043405C:G02	ES 151
M00043406B:G12	ES 151

Clone Name	Tube
M00043407C:E05	ES 151
M00043408B:D11	ES 151
M00043409B:B03	ES 151
M00043410C:A09	ES 151
M00043411B:D08	ES 151
M00043411D:H06	ES 151
M00042584B:C10	ES 151
M00042623D:D07	ES 151
M00042625C:B04	ES 151
M00042626B:D08	ES 151
M00042627C:D01	ES 151
M00042630A:C05	ES 151
M00042955C:D05	ES 151
M00042956C:B06	ES 151
M00042960D:H08	ES 151
M00042962D:C05	ES 151
M00042964D:A03	ES 151
M00042966B:F07	ES 151
M00042966C:E06	ES 151
M00042970C:A04	ES 151
M00042970C:H10	ES 151
M00042976A:H04	ES 151
M00042979B:E02	ES 151
M00042981B:D11	ES 151
M00042983C:A11	ES 151
M00042983C:G06	ES 151
M00042986C:G12	ES 151
M00042988A:F06	ES 151
M00042997B:D06	ES 151
M00042998A:E03	ES 151
M00042998A:G04	ES 151
M00043001B:H10	ES 151
M00043001D:D03	ES 151
M00043002A:E05	ES 151
M00043003C:D08	ES 151
M00043011A:H12	ES 151
M00043015A:H10	ES 151
M00043022A:E12	ES 151
M00043026C:D07	ES 151
M00043028A:G05	ES 151
M00043029C:A06	ES 151
M00043032C:A10	ES 151
M00043034D:C01	ES 151
M00043036C:E05	ES 151
M00043036D:C09	ES 151

Clone Name	Tube
M00043040B:B07	ES 151
M00043044B:A12	ES 151
M00043044D:A09	ES 151
M00043045D:G12	ES 151
M00043046D:B11	ES 151
M00043060D:G12	ES 151
M00043066B:H11	ES 151
M00043067D:D10	ES 151
M00043125A:B11	ES 151
M00043125C:A11	ES 151
M00042611A:A06	ES 151
M00042611D:B12	ES 151
M00042612D:F06	ES 151
M00042614B:B05	ES 151
M00043073A:C12	ES 151
M00043078D:D04	ES 151
M00043081D:F05	ES 151
M00043087B:G07	ES 151
M00043093C:G11	ES 151
M00043095A:F09	ES 152
M00043096A:G04	ES 152
M00043108A:F06	ES 152
M00043109C:G01	ES 152
M00043131B:A09	ES 152
M00043133B:C11	ES 152
M00043138D:B11	ES 152
M00043143B:A10	ES 152
M00043148C:A09	ES 152
M00043154A:B07	ES 152
M00043162A:B08	ES 152
M00043162D:C12	ES 152
M00043164C:E12	ES 152
M00043165B:G01	ES 152
M00043173D:G03	ES 152
M00043184A:H08	ES 152
M00043187A:C04	ES 152
M00043191A:A07	ES 152
M00043192C:B12	ES 152
M00043200A:H09	ES 152
M00043200B:C08	ES 152
M00043202B:F01	ES 152
M00043203A:B09	ES 152
M00043210C:E05	ES 152
M00043211A:F01	ES 152
M00043213B:B12	ES 152

Clone Name	Tube
M00043215A:D02	ES 152
M00043220B:C04	ES 152
M00042591D:H03	ES 152
M00042592A:H10	ES 152
M00042593A:C02	ES 152
M00042593C:G06	ES 152
M00042595A:A11	ES 152
M00042595A:B01	ES 152
M00042596B:F06	ES 152
M00042596C:D07	ES 152
M00042597B:E12	ES 152
M00043416C:A02	ES 152
M00043417C:D05	ES 152
M00043418A:H10	ES 152
M00043419D:A10	ES 152
M00043428D:G08	ES 152
M00043430B:C02	ES 152
M00043431D:B08	ES 152
M00043433B:G09	ES 152
M00043433C:G07	ES 152
M00043437D:D04	ES 152
M00043440C:B07	ES 152
M00043446C:E12	ES 152
M00043447A:C07	ES 152
M00043449A:E12	ES 152
M00043450C:C06	ES 152
M00043453B:B09	ES 152
M00043458A:B12	ES 152
M00043461D:C02	ES 152
M00043461D:E06	ES 152
M00043465B:H02	ES 152
M00043465C:A03	ES 152
M00043465C:C09	ES 152
M00043476A:F07	ES 152
M00043483B:G10	ES 152
M00043491C:F04	ES 152
M00043492A:E01	ES 152
M00043513D:G08	ES 152
M00043516B:H09	ES 152
M00043518B:D06	ES 152
M00043526B:D10	ES 152
M00043527C:E09	ES 152
M00043528C:A02	ES 152
M00043616B:F02	ES 152
M00043616C:A05	ES 152

Clone Name	Tube
M00043632D:F09	ES 152
M00043634A:C10	ES 152
M00043635C:C11	ES 152
M00043636B:C06	ES 152
M00043637C:H01	ES 152
M00043638A:D06	ES 152
M00043640C:E03	ES 152
M00043648A:G07	ES 152
M00043649B:E07	ES 152
M00001338C:B02	ES 153
M00001338C:F05	ES 153
M00001338D:D01	ES 153
M00001340D:F07	ES 153
M00001344D:E08	ES 153
M00001346B:G11	ES 153
M00001348B:B03	ES 153
M00001349C:B04	ES 153
M00001351B:E11	ES 153
M00001352B:B02	ES 153
M00001353A:H07	ES 153
M00001353C:A05	ES 153
M00001353D:E05	ES 153
M00001356D:E06	ES 153
M00001358A:E08	ES 153
M00001359A:H10	ES 153
M00001361A:C12	ES 153
M00001361B:A12	ES 153
M00001362A:F09	ES 153
M00001364A:C09	ES 153
M00001364C:H10	ES 153
M00001368A:A08	ES 153
M00001368A:B07	ES 153
M00001368A:C02	ES 153
M00001369A:G06	ES 153
M00001374A:B02	ES 153
M00001374C:B10	ES 153
M00001375B:D04	ES 153
M00001378C:E10	ES 153
M00001379A:F09	ES 153
M00001382D:A07	ES 153
M00001382D:H08	ES 153
M00001384A:A07	ES 153
M00001385A:E07	ES 153
M00001386B:F11	ES 153
M00001387A:C12	ES 153
M00001387B:A11	ES 153
M00001389B:E10	ES 153
M00001389D:D06	ES 153

Clone Name	Tube
M00001390D:E02	ES 153
M00001391D:D03	ES 153
M00001393B:C03	ES 153
M00001393C:E08	ES 153
M00001393C:F04	ES 153
M00001393D:E02	ES 153
M00001396B:B01	ES 153
M00001396B:B12	ES 153
M00001396D:H02	ES 153
M00001397C:H08	ES 153
M00001399B:B01	ES 153
M00001399C:A01	ES 153
M00001403C:B03	ES 153
M00001403D:C12	ES 153
M00001406B:H09	ES 153
M00001406D:F06	ES 153
M00001410A:G10	ES 153
M00001416B:A05	ES 153
M00001421B:E07	ES 153
M00001422B:D06	ES 153
M00001424B:H06	ES 153
M00001424D:D02	ES 153
M00001426C:F06	ES 153
M00001428B:C10	ES 153
M00001429B:G05	ES 153
M00001430B:C01	ES 153
M00001433B:E02	ES 153
M00001442A:F08	ES 153
M00001442C:G12	ES 153
M00001444B:E04	ES 153
M00001444C:D11	ES 153
M00001445B:F06	ES 153
M00001449B:H10	ES 153
M00001451C:E10	ES 153
M00001460C:E10	ES 153
M00001461D:B10	ES 153
M00001461D:C10	ES 153
M00001465C:A02	ES 153
M00001466B:F03	ES 153
M00001467C:D04	ES 153
M00001477D:G09	ES 153
M00001485C:F06	ES 153
M00001488C:A03	ES 153
M00001497C:F10	ES 153
M00001503B:H10	ES 153
M00001506B:D11	ES 153
M00001512D:F08	ES 153
M00001518B:D10	ES 153
M00001528C:C03	ES 153

Clone Name	Tube
M00001532A:G08	ES 153
M00001533C:G11	ES 153
M00001533D:A01	ES 153
M00001534C:E07	ES 153
M00001535B:B10	ES 153
M00001535B:E02	ES 153
M00001537B:H10	ES 153
M00001538B:A07	ES 153
M00001539C:F12	ES 154
M00001542B:F09	ES 154
M00001543C:A08	ES 154
M00001544B:B05	ES 154
M00001544B:E06	ES 154
M00001546B:C11	ES 154
M00001548B:D06	ES 154
M00001550A:H06	ES 154
M00001550D:B11	ES 154
M00001551D:D01	ES 154
M00001551D:H09	ES 154
M00001554C:G10	ES 154
M00001558A:E06	ES 154
M00001559A:H09	ES 154
M00001561D:H04	ES 154
M00001562B:B02	ES 154
M00001562D:B07	ES 154
M00001565A:H05	ES 154
M00001568C:A03	ES 154
M00001570A:B07	ES 154
M00001591B:H05	ES 154
M00001596A:D02	ES 154
M00001600B:G01	ES 154
M00001605B:B05	ES 154
M00001606B:A10	ES 154
M00001606D:D06	ES 154
M00001607A:E04	ES 154
M00001607D:H09	ES 154
M00001609D:C11	ES 154
M00001616D:F03	ES 154
M00001617C:F10	ES 154
M00001618C:D01	ES 154
M00001619C:H09	ES 154
M00001620B:A03	ES 154
M00001623D:A10	ES 154
M00001623D:E12	ES 154
M00001624A:C01	ES 154
M00001625D:B04	ES 154
M00001626A:D07	ES 154
M00001632C:A10	ES 154
M00001633D:C11	ES 154

Clone Name	Tube
M00001637D:C12	ES 154
M00001648A:D10	ES 154
M00001661D:F06	ES 154
M00001663A:A12	ES 154
M00001671A:H10	ES 154
M00001671C:F03	ES 154
M00001675B:D06	ES 154
M00001677B:H08	ES 154
M00001680A:A01	ES 154
M00001683B:F11	ES 154
M00001684D:E04	ES 154
M00001686B:H01	ES 154
M00001686D:F06	ES 154
M00001688B:B11	ES 154
M00001692C:C04	ES 154
M00001771B:E06	ES 154
M00003746C:E11	ES 154
M00003749C:C08	ES 154
M00003753A:C11	ES 154
M00003758B:D07	ES 154
M00003758B:F06	ES 154
M00003760C:G10	ES 154
M00003761B:B02	ES 154
M00003763A:B02	ES 154
M00003763B:B10	ES 154
M00003764A:H09	ES 154
M00003764B:F11	ES 154
M00003764B:H11	ES 154
M00003764D:F07	ES 154
M00003768D:D08	ES 154
M00003770C:A10	ES 154
M00003771D:A03	ES 154
M00003773A:F10	ES 154
M00003780A:G01	ES 154
M00003782A:B02	ES 154
M00003785D:F07	ES 154
M00003787D:A10	ES 154
M00003808A:F11	ES 154
M00003808B:E07	ES 154
M00003812C:A03	ES 154
M00003814A:G05	ES 154
M00003819B:B01	ES 154
M00003820B:F11	ES 154
M00003821C:E12	ES 154
M00003822C:A09	ES 154
M00003822D:A02	ES 154
M00003823B:A06	ES 154
M00003825A:H10	ES 154
M00003828A:D11	ES 154

Clone Name	Tube
M00003830B:C06	ES 154
M00003830C:D02	ES 154
M00003837C:D10	ES 154
M00003839C:H10	ES 154
M00003842D:D11	ES 154
M00003842D:H09	ES 154
M00003845A:C07	ES 155
M00003845D:G03	ES 155
M00003847A:H04	ES 155
M00003848C:G09	ES 155
M00003851B:A01	ES 155
M00003854B:F07	ES 155
M00003855C:F02	ES 155
M00003884A:E12	ES 155
M00003887C:E09	ES 155
M00003888B:F09	ES 155
M00003891B:H02	ES 155
M00003898C:A01	ES 155
M00003900C:D12	ES 155
M00003906A:C02	ES 155
M00003911C:A09	ES 155
M00003914A:A08	ES 155
M00003915C:D10	ES 155
M00003915C:G08	ES 155
M00003916A:E04	ES 155
M00003926A:F11	ES 155
M00003935B:B01	ES 155
M00003938C:A05	ES 155
M00003942A:D01	ES 155
M00003958C:H08	ES 155
M00003959D:A05	ES 155
M00003960D:C12	ES 155
M00003963D:F01	ES 155
M00003965D:D11	ES 155
M00003968C:G03	ES 155
M00003970D:H07	ES 155
M00003972C:F07	ES 155
M00003974C:E11	ES 155
M00003974D:E02	ES 155
M00003979B:A04	ES 155
M00003980D:C06	ES 155
M00003985D:B02	ES 155
M00003988D:B01	ES 155
M00003991A:C11	ES 155
M00003993C:D07	ES 155
M00003993D:B03	ES 155
M00003994A:B10	ES 155
M00003996B:H07	ES 155
M00003998B:G10	ES 155

Clone Name	Tube
M00004028B:F10	ES 155
M00004029D:A01	ES 155
M00004031C:G06	ES 155
M00004036B:A11	ES 155
M00004036D:C12	ES 155
M00004038A:A04	ES 155
M00004042B:A11	ES 155
M00004047C:B09	ES 155
M00004047D:F12	ES 155
M00004053D:F09	ES 155
M00004054A:D03	ES 155
M00004055C:B10	ES 155
M00004055D:D05	ES 155
M00004057D:G01	ES 155
M00004061B:E05	ES 155
M00004062D:A02	ES 155
M00004066D:G10	ES 155
M00004067B:D03	ES 155
M00004080C:C04	ES 155
M00004085A:H01	ES 155
M00004085B:H02	ES 155
M00004087C:E02	ES 155
M00004093A:C03	ES 155
M00004096D:F02	ES 155
M00004102A:E03	ES 155
M00004103C:E10	ES 155
M00004104A:A12	ES 155
M00004110D:F09	ES 155
M00004114C:D11	ES 155
M00004115A:G12	ES 155
M00004118C:D12	ES 155
M00004122C:D01	ES 155
M00004134A:A08	ES 155
M00004136C:B12	ES 155
M00004139B:F01	ES 155
M00004141A:D01	ES 155
M00004141B:B01	ES 155
M00004141B:F08	ES 155
M00004143B:B04	ES 155
M00004144D:B02	ES 155
M00004146A:C11	ES 155
M00004146B:E08	ES 155
M00004146C:B04	ES 155
M00004147C:E01	ES 155
M00004151B:A07	ES 155
M00004155A:H03	ES 155
M00004155C:A10	ES 155
M00004158B:E03	ES 155
M00004158D:E08	ES 155

Clone Name	Tube
M00004159C:D10	ES 155
M00004159D:F12	ES 155
M00004160D:F06	ES 155
M00004160D:G05	ES 155
M00004162D:F02	ES 156
M00004163B:C03	ES 156
M00004163C:A03	ES 156
M00004164B:E12	ES 156
M00004165C:A11	ES 156
M00004166C:B10	ES 156
M00004169A:E04	ES 156
M00004170A:F03	ES 156
M00004171B:B03	ES 156
M00004172C:A08	ES 156
M00004172D:B12	ES 156
M00004172D:F04	ES 156
M00004175D:E06	ES 156
M00004176C:A09	ES 156
M00004179C:B06	ES 156
M00004179D:A12	ES 156
M00004187B:C02	ES 156
M00004189A:C12	ES 156
M00004192C:B06	ES 156
M00004195A:F07	ES 156
M00004200C:A04	ES 156
M00004201D:C01	ES 156
M00004201D:C03	ES 156
M00004204C:H08	ES 156
M00004207C:A04	ES 156
M00004208A:D08	ES 156
M00004210A:A03	ES 156
M00004212D:C03	ES 156
M00004214A:E05	ES 156
M00004214D:A05	ES 156
M00004215B:C05	ES 156
M00004220D:C11	ES 156
M00004225D:E03	ES 156
M00004229B:B06	ES 156
M00004230D:B05	ES 156
M00004237C:D10	ES 156
M00004242D:H01	ES 156
M00004245C:G10	ES 156
M00004246B:H07	ES 156
M00004251D:D03	ES 156
M00004263C:D03	ES 156
M00004266B:F07	ES 156
M00004269A:F11	ES 156
M00004269A:G11	ES 156
M00004269B:B04	ES 156

Clone Name	Tube
M00004270A:E09	ES 156
M00004276C:A08	ES 156
M00004277D:B02	ES 156
M00004278A:G06	ES 156
M00004278C:B10	ES 156
M00004281A:C04	ES 156
M00004282A:D01	ES 156
M00004282B:D07	ES 156
M00004282C:A12	ES 156
M00004284A:F08	ES 156
M00004295D:C07	ES 156
M00004296B:D03	ES 156
M00004303C:C05	ES 156
M00004310B:E02	ES 156
M00004316A:B03	ES 156
M00004320C:E07	ES 156
M00004321C:C11	ES 156
M00004322B:D03	ES 156
M00004324A:B03	ES 156
M00004324A:D10	ES 156
M00004324A:D05	ES 156
M00004328A:D01	ES 156
M00004330A:A01	ES 156
M00004336A:A01	ES 156
M00004341C:A09	ES 156
M00004341C:E05	ES 156
M00004344A:G11	ES 156
M00004344D:C12	ES 156
M00004347B:E04	ES 156
M00004347C:A05	ES 156
M00004350A:A04	ES 156
M00004351B:G07	ES 156
M00004352A:D08	ES 156
M00004357B:B06	ES 156
M00004358B:G02	ES 156
M00004359A:E01	ES 156
M00004360C:D09	ES 156
M00004365C:C09	ES 156
M00004365C:G11	ES 156
M00004366D:C11	ES 156
M00004368A:B11	ES 156
M00004372A:E12	ES 156
M00004376D:A12	ES 156
M00004385C:H12	ES 156
M00004393C:D06	ES 156
M00004406A:G09	ES 156
M00004416B:G10	ES 156
M00004418B:A11	ES 156
M00004419A:G02	ES 156

Clone Name	Tube
M00004420D:E05	ES 156
M00004430A:A05	ES 156
M00004430B:B10	ES 157
M00004443C:F07	ES 157
M00004462D:D12	ES 157
M00004502A:D12	ES 157
M00004507D:E03	ES 157
M00004509B:B10	ES 157
M00004509D:C06	ES 157
M00004603B:E02	ES 157
M00004603C:C10	ES 157
M00004606D:H09	ES 157
M00004608A:C10	ES 157
M00004608A:H04	ES 157
M00004609A:E09	ES 157
M00023389A:G04	ES 157
M00023394D:D10	ES 157
M00026809A:H08	ES 157
M00026818C:E01	ES 157
M00026836B:H03	ES 157
M00026842B:A01	ES 157
M00026842D:C02	ES 157
M00026850B:C09	ES 157
M00026856B:G03	ES 157
M00026900A:H07	ES 157
M00026907D:E07	ES 157
M00026910B:G06	ES 157
M00026914C:H09	ES 157
M00026936D:C07	ES 157
M00026961A:B06	ES 157
M00026994D:D07	ES 157
M00027004C:C11	ES 157
M00027017A:B09	ES 157
M00027036A:B06	ES 157
M00027050A:B02	ES 157
M00027052A:E10	ES 157
M00027057C:D10	ES 157
M00027064B:D06	ES 157
M00027081A:A08	ES 157
M00027093A:H02	ES 157
M00027131A:B03	ES 157
M00027159C:F07	ES 157
M00027167C:B10	ES 157
M00027168B:H08	ES 157
M00027170D:C07	ES 157
M00027173C:E11	ES 157
M00027177B:D04	ES 157
M00027178B:A11	ES 157
M00027182B:G06	ES 157

Clone Name	Tube
M00027189C:B10	ES 157
M00027193C:A07	ES 157
M00027215A:F06	ES 157
M00027215B:B12	ES 157
M00027244C:B06	ES 157
M00027247C:D02	ES 157
M00027262A:A07	ES 157
M00027270A:D04	ES 157
M00027274A:A09	ES 157
M00027290C:F06	ES 157
M00027291A:G08	ES 157
M00027311A:H09	ES 157
M00027313C:E01	ES 157
M00027314D:E02	ES 157
M00027316C:C03	ES 157
M00027319C:C03	ES 157
M00027319D:F07	ES 157
M00027332B:H09	ES 157
M00027359B:A06	ES 157
M00027363D:G04	ES 157
M00027364B:E12	ES 157
M00027376C:A02	ES 157
M00027381B:B04	ES 157
M00027400D:H02	ES 157
M00027433B:D12	ES 157
M00027457B:E11	ES 157
M00027459C:B10	ES 157
M00027467A:C07	ES 157
M00027475D:A01	ES 157
M00027480C:E09	ES 157
M00027485C:F07	ES 157
M00027506B:G01	ES 157
M00027513D:F06	ES 157
M00027523A:H05	ES 157
M00027527B:C05	ES 157
M00027549C:G03	ES 157
M00027569A:E05	ES 157
M00027586A:C09	ES 157
M00027589B:G07	ES 157
M00027591A:E04	ES 157
M00027600B:C07	ES 157
M00027605B:D09	ES 157
M00027688C:C01	ES 157
M00027717C:C06	ES 157
M00027724D:D04	ES 157
M00027734D:C03	ES 157
M00027746A:D06	ES 157
M00027801B:D07	ES 157
M00027806C:H05	ES 157

Clone Name	Tube
M00028055B:G07	ES 158
M00028063C:H01	ES 158
M00028067A:C11	ES 158
M00028069D:H02	ES 158
M00028070A:H09	ES 158
M00028070D:C03	ES 158
M00028188C:H11	ES 158
M00028193B:E07	ES 158
M00028196A:G03	ES 158
M00028210B:H03	ES 158
M00028211A:F10	ES 158
M00028212D:C05	ES 158
M00028219B:H05	ES 158
M00028361B:H08	ES 158
M00028366B:B08	ES 158
M00028616C:D09	ES 158
M00028620C:C07	ES 158
M00028763A:G11	ES 158
M00028764B:D03	ES 158
M00028771A:E02	ES 158
M00028773C:C05	ES 158
M00028774D:E10	ES 158
M00028777B:G04	ES 158
M00028782A:F01	ES 158
M00028784A:D12	ES 158
M00028786B:A04	ES 158
M00031370B:C01	ES 158
M00031416D:H05	ES 158
M00031484A:D03	ES 158
M00031485B:G05	ES 158
M00032471D:A05	ES 158
M00032473B:A03	ES 158
M00032474A:G03	ES 158
M00032475A:A06	ES 158
M00032489B:G12	ES 158
M00032490D:E08	ES 158
M00032494C:H08	ES 158
M00032497D:B10	ES 158
M00032504B:B10	ES 158
M00032507D:G08	ES 158
M00032508A:E03	ES 158
M00032515A:B12	ES 158
M00032517C:E10	ES 158
M00032519D:F08	ES 158
M00032534B:E12	ES 158

Clone Name	Tube
M00032541C:G03	ES 158
M00032553A:A07	ES 158
M00032556D:A03	ES 158
M00032562C:F01	ES 158
M00032567B:G05	ES 158
M00032568B:F08	ES 158
M00032577D:F01	ES 158
M00032580D:A09	ES 158
M00032581B:A09	ES 158
M00032584A:D06	ES 158
M00032586C:B04	ES 158
M00032590B:H01	ES 158
M00032594C:F05	ES 158
M00032597A:H02	ES 158
M00032605B:D09	ES 158
M00032613A:E11	ES 158
M00032614C:B10	ES 158
M00032614D:D08	ES 158
M00032620B:F06	ES 158
M00032621A:F11	ES 158
M00032628C:B06	ES 158
M00032634B:D09	ES 158
M00032637A:F09	ES 158
M00032638B:F02	ES 158
M00032644C:B05	ES 158
M00032645D:C01	ES 158
M00032647B:F06	ES 158
M00032652C:C07	ES 158
M00032666A:C02	ES 158
M00032671B:D06	ES 158
M00032671B:D08	ES 158
M00032676C:C10	ES 158
M00032688C:A03	ES 158
M00032700A:E09	ES 158
M00032707D:F08	ES 158
M00032711B:F01	ES 158
M00032723D:H02	ES 158
M00032727A:E04	ES 158
M00032728D:F01	ES 158
M00032729A:F10	ES 158
M00032733B:F12	ES 158
M00032734B:E12	ES 158
M00032734C:C05	ES 158
M00032749D:G03	ES 158
M00032753A:C07	ES 158

Clone Name	Tube
M00032759A:A03	ES 158
M00032765A:C05	ES 158
M00032770C:G11	ES 158
M00032772D:D03	ES 158
M00032773D:F08	ES 158
M00032774C:C04	ES 158
M00032787D:C05	ES 159
M00032791B:H11	ES 159
M00032791D:F01	ES 159
M00032792C:B01	ES 159
M00032793A:G06	ES 159
M00032795C:A03	ES 159
M00032797D:D08	ES 159
M00032825B:F08	ES 159
M00032826C:D10	ES 159
M00032828A:A06	ES 159
M00032829D:A05	ES 159
M00032830D:D02	ES 159
M00032831A:C07	ES 159
M00032831A:E09	ES 159
M00032835D:G04	ES 159
M00032836B:A07	ES 159
M00032848D:B10	ES 159
M00032892C:C12	ES 159
M00032908A:D08	ES 159
M00032918D:B04	ES 159
M00032928C:D02	ES 159
M00032944A:B07	ES 159
M00032945D:B07	ES 159
M00032979D:C11	ES 159
M00032979D:H07	ES 159
M00032985D:G09	ES 159
M00032987B:F01	ES 159
M00032988B:G01	ES 159
M00033006A:F10	ES 159
M00033028C:A02	ES 159
M00033028D:C10	ES 159
M00033037B:F04	ES 159
M00033041A:B11	ES 159
M00033055D:D02	ES 159
M00033071C:G05	ES 159
M00033071D:E08	ES 159
M00033072A:A09	ES 159
M00033080C:A07	ES 159
M00033081D:D11	ES 159

Clone Name	Tube
M00033144A:D02	ES 159
M00033146D:A03	ES 159
M00033147C:B08	ES 159
M00033149B:E10	ES 159
M00033150B:E02	ES 159
M00033150C:A11	ES 159
M00033183B:F10	ES 159
M00033218C:F07	ES 159
M00033223C:G04	ES 159
M00033230C:G10	ES 159
M00033232B:C08	ES 159
M00033246A:H12	ES 159
M00033248D:H11	ES 159
M00033264B:E06	ES 159
M00033274D:F03	ES 159
M00033311B:G10	ES 159
M00033324B:F04	ES 159
M00033326B:B05	ES 159
M00033329C:C02	ES 159
M00033296C:C11	ES 159
M00033302A:E11	ES 159
M00033302B:F10	ES 159
M00033303C:F09	ES 159
M00033342B:F03	ES 159
M00033344A:B06	ES 159
M00033359C:H05	ES 159
M00033360C:A03	ES 159
M00033374D:C07	ES 159
M00033413A:A08	ES 159
M00033420B:E08	ES 159
M00033434D:F05	ES 159
M00033441A:B12	ES 159
M00033445D:G03	ES 159
M00038290A:D12	ES 159
M00038304B:E02	ES 159
M00038389D:D10	ES 159
M00038390B:F02	ES 159
M00038616C:C09	ES 159
M00038616D:B07	ES 159
M00038618D:D08	ES 159
M00038619B:F09	ES 159
M00038619D:C12	ES 159
M00039001A:B10	ES 159
M00039024D:E12	ES 159
M00039055C:A01	ES 159

Clone Name	Tube
M00039056B:G01	ES 159
M00039063C:H09	ES 159
M00039067A:C05	ES 159
M00039067B:F07	ES 159
M00039076D:G04	ES 159
M00039078B:B03	ES 159
M00039078D:C10	ES 159
M00039081B:C04	ES 159
M00039081B:G07	ES 159
M00039100A:G04	ES 159
M00039105D:A08	ES 159
M00039107A:E12	ES 159
M00039111A:C12	ES 160
M00039121D:E07	ES 160
M00039124D:H01	ES 160
M00039125D:H12	ES 160
M00039131C:B09	ES 160
M00039133B:D06	ES 160
M00039133C:F12	ES 160
M00039134D:F08	ES 160
M00039138B:G05	ES 160
M00039140A:F05	ES 160
M00039143A:F04	ES 160
M00039143D:C10	ES 160
M00039146B:G04	ES 160
M00039162D:C04	ES 160
M00039165D:C04	ES 160
M00039175A:F01	ES 160
M00039204A:E09	ES 160
M00039207A:F07	ES 160
M00039219B:C08	ES 160
M00039222B:A04	ES 160
M00039225A:D11	ES 160
M00039246B:A08	ES 160
M00039248C:A08	ES 160
M00039251C:H12	ES 160
M00039251D:B08	ES 160
M00039255D:B01	ES 160
M00039258C:C01	ES 160
M00039270D:D02	ES 160
M00039275B:E02	ES 160
M00039278C:D03	ES 160
M00039284D:H07	ES 160
M00039285B:G04	ES 160
M00039291D:F02	ES 160

Clone Name	Tube
M00039294C:B09	ES 160
M00039302B:E10	ES 160
M00039326A:G07	ES 160
M00039326C:B08	ES 160
M00039331B:F09	ES 160
M00039338B:F07	ES 160
M00039344C:A11	ES 160
M00039349D:B11	ES 160
M00039381C:C07	ES 160
M00039383A:H07	ES 160
M00039411D:D09	ES 160
M00039413C:E06	ES 160
M00039430A:E04	ES 160
M00039433B:D06	ES 160
M00039433C:E03	ES 160
M00039438B:D08	ES 160
M00039440C:G06	ES 160
M00039457D:C02	ES 160
M00039471D:G10	ES 160
M00039472B:E05	ES 160
M00039478C:B02	ES 160
M00039554D:B09	ES 160
M00039556C:G05	ES 160
M00039559B:C07	ES 160
M00039560B:G09	ES 160
M00039560C:G06	ES 160
M00039617C:A10	ES 160
M00039654C:C11	ES 160
M00039668C:F01	ES 160
M00039672C:D05	ES 160
M00039686C:C01	ES 160
M00039694C:H01	ES 160
M00039698C:B03	ES 160
M00039710B:A01	ES 160
M00039710B:E01	ES 160
M00039785C:H12	ES 160
M00039786D:A10	ES 160
M00039805B:B06	ES 160
M00039806B:D05	ES 160
M00039820B:F06	ES 160
M00039822A:H02	ES 160
M00039826B:F09	ES 160
M00039826D:E04	ES 160
M00039828B:H06	ES 160
M00039829B:E01	ES 160

Clone Name	Tube
M00039860B:E01	ES 160
M00039860D:B02	ES 160
M00039861C:B12	ES 160
M00039865A:C09	ES 160
M00039869A:H01	ES 160
M00039871C:G05	ES 160
M00039873B:H04	ES 160
M00039874A:B06	ES 160
M00039885C:D11	ES 160
M00039894C:D09	ES 160
M00039895D:C04	ES 160
M00039900B:G04	ES 160
M00039915B:E08	ES 160
M00039921A:B10	ES 160
M00004824A:D12	ES 160
M00004824D:H05	ES 160
M00004831C:G11	ES 160
M00004832D:G04	ES 160
M00004836B:C02	ES 161
M00004839B:C12	ES 161
M00004843A:G12	ES 161
M00004846A:A10	ES 161
M00004850A:B02	ES 161
M00004852D:C06	ES 161
M00004856D:F09	ES 161
M00004873B:G04	ES 161
M00004876B:A06	ES 161
M00005002A:C03	ES 161
M00005003D:C02	ES 161
M00005013D:H05	ES 161
M00005014B:F02	ES 161
M00005016C:E04	ES 161
M00005309B:A11	ES 161
M00005314A:G10	ES 161
M00005332A:C06	ES 161
M00005333D:D08	ES 161
M00005346D:A03	ES 161
M00005349C:C02	ES 161
M00005359B:B08	ES 161
M00005359B:D09	ES 161
M00005364B:E10	ES 161
M00005365A:F05	ES 161
M00005366D:F08	ES 161
M00005367D:A11	ES 161
M00005375D:A10	ES 161

Clone Name	Tube
M00005379A:D10	ES 161
M00005380B:H10	ES 161
M00005383A:C11	ES 161
M00005385A:B12	ES 161
M00005385D:F07	ES 161
M00005387A:B03	ES 161
M00005392A:G06	ES 161
M00005401D:F09	ES 161
M00005403C:A01	ES 161
M00005405C:D01	ES 161
M00005409D:B02	ES 161
M00005413D:A05	ES 161
M00005422B:B08	ES 161
M00005422D:H02	ES 161
M00005422D:H10	ES 161
M00005423A:C11	ES 161
M00005423C:A10	ES 161
M00005423C:D07	ES 161
M00005434A:C03	ES 161
M00005442A:B10	ES 161
M00005445A:E07	ES 161
M00005445D:D04	ES 161
M00005445D:F11	ES 161
M00005452B:G03	ES 161
M00005452D:E05	ES 161
M00005460D:C11	ES 161
M00005461A:D12	ES 161
M00005463A:G02	ES 161
M00005466C:B01	ES 161
M00005468A:C04	ES 161
M00005468D:C01	ES 161
M00005474C:H09	ES 161
M00005485C:H04	ES 161
M00005489B:C08	ES 161
M00005500A:D04	ES 161
M00005504C:F12	ES 161
M00005504D:F06	ES 161
M00005505A:F01	ES 161
M00005505B:E01	ES 161
M00005506C:E09	ES 161
M00005506D:E11	ES 161
M00005507B:A03	ES 161
M00005511A:F05	ES 161
M00005512B:H01	ES 161
M00005515D:F02	ES 161

Clone Name	Tube
M00005520B:E01	ES 161
M00005520B:H05	ES 161
M00005524C:H04	ES 161
M00005535B:B01	ES 161
M00005540A:F09	ES 161
M00005557D:H10	ES 161
M00005569D:G09	ES 161
M00005570A:B08	ES 161
M00005570A:D05	ES 161
M00005603B:H03	ES 161
M00005606D:B12	ES 161
M00005607B:C04	ES 161
M00005616B:F07	ES 161
M00005622A:H02	ES 161
M00005623B:G01	ES 161
M00005626D:G11	ES 161
M00005634A:F07	ES 161
M00005641B:E09	ES 161
M00005643D:A05	ES 161
M00005674C:F04	ES 161
M00005675D:D09	ES 161
M00005689C:B02	ES 161
M00005703B:E03	ES 161
M00005703D:G10	ES 161
M00005710B:H03	ES 162
M00005743D:A12	ES 162
M00005763D:A01	ES 162
M00005766D:D12	ES 162
M00005771D:C02	ES 162
M00005819D:F09	ES 162
M00005822C:A04	ES 162
M00006576D:C02	ES 162
M00006577A:H10	ES 162
M00006582D:A09	ES 162
M00006585A:D07	ES 162
M00006585A:F09	ES 162
M00006586D:D04	ES 162
M00006592A:A12	ES 162
M00006595B:C10	ES 162
M00006601D:G05	ES 162
M00006631C:A04	ES 162
M00006631D:D02	ES 162
M00006636B:E04	ES 162
M00006641B:F05	ES 162
M00006646A:A07	ES 162

Clone Name	Tube
M00006678A:A03	ES 162
M00006678C:C02	ES 162
M00006712C:H01	ES 162
M00006714C:D06	ES 162
M00006738A:F12	ES 162
M00006739B:A04	ES 162
M00006740B:A09	ES 162
M00006743A:D04	ES 162
M00006743A:H11	ES 162
M00006756B:G06	ES 162
M00006756C:A02	ES 162
M00006861D:H10	ES 162
M00006872D:B07	ES 162
M00006877B:C09	ES 162
M00006877C:F11	ES 162
M00006884D:A08	ES 162
M00006885A:F07	ES 162
M00006890C:F10	ES 162
M00006904D:A02	ES 162
M00006907A:C09	ES 162
M00006907B:C06	ES 162
M00006989B:G05	ES 162
M00006994C:F06	ES 162
M00007002C:A10	ES 162
M00007006C:C12	ES 162
M00007007A:E04	ES 162
M00007031A:E02	ES 162
M00007032A:B05	ES 162
M00007032C:A12	ES 162
M00007046D:C09	ES 162
M00007048B:E11	ES 162
M00007048C:A12	ES 162
M00007059B:D07	ES 162
M00007060D:G07	ES 162
M00007064D:D12	ES 162
M00007070C:C01	ES 162
M00007081B:C08	ES 162
M00007081B:E09	ES 162
M00007082D:E05	ES 162
M00007098A:E10	ES 162
M00007103C:C12	ES 162
M00007103D:C02	ES 162
M00007112D:D03	ES 162
M00007117A:C11	ES 162
M00007126A:A02	ES 162

Clone Name	Tube
M00007141C:B05	ES 162
M00007154A:E06	ES 162
M00007155C:D07	ES 162
M00007155D:C09	ES 162
M00007158D:D03	ES 162
M00007178A:C02	ES 162
M00007195C:E11	ES 162
M00007197B:B05	ES 162
M00007202B:F01	ES 162
M00007947A:B06	ES 162
M00007953D:F07	ES 162
M00007969D:C01	ES 162
M00007973B:D11	ES 162
M00007975C:A10	ES 162
M00007975D:F12	ES 162
M00007980A:B01	ES 162
M00007980B:A07	ES 162
M00007981C:F07	ES 162
M00007985C:D08	ES 162
M00008001B:F05	ES 162
M00008007B:E03	ES 162
M00008016B:E09	ES 162
M00008019B:A01	ES 162
M00008020D:D05	ES 162
M00008020D:F02	ES 162
M00008021C:G12	ES 162
M00008045C:A05	ES 162
M00008055D:G03	ES 162
M00008059B:F08	ES 162
M00008059D:B08	ES 162
M00008065D:A07	ES 163
M00008071D:H03	ES 163
M00008073A:D01	ES 163
M00008073D:D01	ES 163
M00021649B:A02	ES 163
M00021650D:A11	ES 163
M00021653A:B02	ES 163
M00021668D:A03	ES 163
M00021676C:G03	ES 163
M00021677A:D09	ES 163
M00021678A:H03	ES 163
M00021678D:H04	ES 163
M00021681C:C09	ES 163
M00021690A:C03	ES 163
M00021697C:B07	ES 163

Clone Name	Tube
M00021700D:H03	ES 163
M00021852C:H02	ES 163
M00021855D:F10	ES 163
M00021866C:H08	ES 163
M00021896D:A05	ES 163
M00021923A:B12	ES 163
M00021923D:H02	ES 163
M00021933B:F02	ES 163
M00021941A:D09	ES 163
M00021952B:G06	ES 163
M00021958B:E08	ES 163
M00021967D:H06	ES 163
M00021971C:B11	ES 163
M00021974D:F01	ES 163
M00021981A:C02	ES 163
M00021991D:F09	ES 163
M00021998B:D09	ES 163
M00022009C:A08	ES 163
M00022016B:F01	ES 163
M00022032A:G05	ES 163
M00022051B:D07	ES 163
M00022069D:C12	ES 163
M00022070B:B04	ES 163
M00022073C:C07	ES 163
M00022081A:B07	ES 163
M00022088B:F10	ES 163
M00022088B:H02	ES 163
M00022088D:E10	ES 163
M00022090B:A10	ES 163
M00022092D:A11	ES 163
M00022094B:G02	ES 163
M00022096D:A03	ES 163
M00022103C:D05	ES 163
M00022104A:G08	ES 163
M00022117C:A02	ES 163
M00022118A:E06	ES 163
M00022140D:A07	ES 163
M00022144C:E12	ES 163
M00022158B:B09	ES 163
M00022170C:C01	ES 163
M00022171A:F03	ES 163
M00022185A:B03	ES 163
M00022193B:A09	ES 163
M00022193C:C09	ES 163
M00022200B:B05	ES 163

Clone Name	Tube
M00022202C:C04	ES 163
M00022208B:D03	ES 163
M00022208C:E04	ES 163
M00022208C:F08	ES 163
M00022212D:G02	ES 163
M00022216D:D10	ES 163
M00022218B:B12	ES 163
M00022220A:A07	ES 163
M00022224A:C07	ES 163
M00022224A:G07	ES 163
M00022228B:B11	ES 163
M00022229D:E01	ES 163
M00022237C:E04	ES 163
M00022237D:D06	ES 163
M00022238C:G04	ES 163
M00022240B:C12	ES 163
M00022240D:B11	ES 163
M00022249D:C01	ES 163
M00022250A:B04	ES 163
M00022262A:F06	ES 163
M00022262B:B06	ES 163
M00022264A:B02	ES 163
M00022265A:F11	ES 163
M00022269C:A04	ES 163
M00022273A:E03	ES 163
M00022282B:C09	ES 163
M00022305A:B04	ES 163
M00022363C:D05	ES 163
M00022367D:G11	ES 163
M00022368A:B11	ES 163
M00022372D:H12	ES 163
M00022374C:E11	ES 163
M00022376D:D05	ES 163
M00022383C:A12	ES 163
M00022386D:F10	ES 163
M00022392B:F01	ES 163
M00022403C:E12	ES 164
M00022415C:D12	ES 164
M00022416D:D01	ES 164
M00022421A:F12	ES 164
M00022425A:C09	ES 164
M00022430C:C06	ES 164
M00022435B:G12	ES 164
M00022436C:F11	ES 164
M00022438C:H09	ES 164

Clone Name	Tube
M00022442B:G03	ES 164
M00022446C:H06	ES 164
M00022449D:F08	ES 164
M00022452B:E06	ES 164
M00022454C:B08	ES 164
M00022457A:G05	ES 164
M00022467D:B03	ES 164
M00022470D:B02	ES 164
M00022472D:B01	ES 164
M00022474B:C08	ES 164
M00022475D:C07	ES 164
M00022481B:A04	ES 164
M00022485B:E07	ES 164
M00022487B:A08	ES 164
M00022487C:C02	ES 164
M00022491A:A08	ES 164
M00022491D:A10	ES 164
M00022494B:D06	ES 164
M00022494D:A05	ES 164
M00022499D:D08	ES 164
M00022507C:C08	ES 164
M00022509A:H02	ES 164
M00022509B:D11	ES 164
M00022512B:A09	ES 164
M00022516B:C05	ES 164
M00022525B:D09	ES 164
M00022530B:C04	ES 164
M00022537B:C06	ES 164
M00022546B:E05	ES 164
M00022559D:G10	ES 164
M00022563B:C08	ES 164
M00022590B:E05	ES 164
M00022600D:B05	ES 164
M00022601B:G06	ES 164
M00022618B:D09	ES 164
M00022618C:E04	ES 164
M00022627B:H03	ES 164
M00022634A:C07	ES 164
M00022634B:H09	ES 164
M00022638A:D03	ES 164
M00022642A:G08	ES 164
M00022648A:D08	ES 164
M00022656D:D07	ES 164
M00022662C:H04	ES 164
M00022662D:H03	ES 164

Clone Name	Tube
M00022672C:H04	ES 164
M00022674C:H08	ES 164
M00022677C:C01	ES 164
M00022678B:C08	ES 164
M00022681D:E10	ES 164
M00022682D:A10	ES 164
M00022684A:E06	ES 164
M00022690A:A07	ES 164
M00022694A:F05	ES 164
M00022696B:C11	ES 164
M00039921C:H11	ES 164
M00039929B:E06	ES 164
M00039929D:H10	ES 164
M00039932B:A07	ES 164
M00039976C:F11	ES 164
M00039977B:D12	ES 164
M00039981D:B01	ES 164
M00040003A:G10	ES 164
M00040016C:E07	ES 164
M00040023B:B10	ES 164
M00040025A:B04	ES 164
M00040034A:E06	ES 164
M00040034B:G02	ES 164
M00040041A:G08	ES 164
M00040041D:F01	ES 164
M00040045B:H07	ES 164
M00040061C:C08	ES 164
M00040075B:A05	ES 164
M00040078A:C07	ES 164
M00040079B:F06	ES 164
M00040079D:D09	ES 164
M00040081C:E02	ES 164
M00040094B:C08	ES 164
M00040118D:C05	ES 164
M00040123C:A10	ES 164
M00040127C:D02	ES 164
M00022698C:D10	ES 164
M00022702D:E02	ES 164
M00022703D:B11	ES 164
M00022706D:G08	ES 164
M00022727A:G01	ES 164
M00022738D:G08	ES 164
M00022740C:H11	ES 165
M00022797D:A06	ES 165
M00022801D:D09	ES 165

Clone Name	Tube
M00022805B:A10	ES 165
M00022812A:G01	ES 165
M00022820A:F07	ES 165
M00022835C:A09	ES 165
M00022854C:G07	ES 165
M00022856D:A07	ES 165
M00022857B:A09	ES 165
M00022897B:F06	ES 165
M00022901A:C05	ES 165
M00022904C:D04	ES 165
M00022924B:A05	ES 165
M00022924C:F04	ES 165
M00022945A:H09	ES 165
M00022945B:F11	ES 165
M00022947B:D02	ES 165
M00022952A:B02	ES 165
M00022953B:D06	ES 165
M00022964A:B03	ES 165
M00022972C:E05	ES 165
M00022992A:H06	ES 165
M00022992B:G12	ES 165
M00022995C:G07	ES 165
M00023004C:A01	ES 165
M00023007D:D03	ES 165
M00023020C:H03	ES 165
M00023097D:B08	ES 165
M00039184D:H09	ES 165
M00039364D:E05	ES 165
M00039377B:E05	ES 165
M00039377B:H09	ES 165
M00039483A:D10	ES 165
M00039526A:A08	ES 165
M00039537A:F08	ES 165
M00039564D:D04	ES 165
M00039594C:B06	ES 165
M00039598A:E04	ES 165
M00039630D:B07	ES 165
M00039642A:A08	ES 165
M00039642C:F08	ES 165
M00039646A:E06	ES 165
M00039647A:A02	ES 165
M00039647B:A02	ES 165
M00039739B:H12	ES 165
M00040132A:H09	ES 165
M00040162A:E02	ES 165

Clone Name	Tube
M00040169A:G06	ES 165
M00040173D:A04	ES 165
M00040174D:G06	ES 165
M00040198A:F12	ES 165
M00040224C:F06	ES 165
M00040247D:D02	ES 165
M00040252C:G05	ES 165
M00040267D:A12	ES 165
M00040287A:C11	ES 165
M00040287C:F10	ES 165
M00040289D:C06	ES 165
M00039747B:B06	ES 165
M00039748C:G09	ES 165
M00040201A:H01	ES 165
M00040219B:B07	ES 165
M00040291A:G10	ES 165
M00040298B:B09	ES 165
M00040314B:D07	ES 165
M00040326B:G09	ES 165
M00040329A:H05	ES 165
M00040338A:B10	ES 165
M00040344C:D05	ES 165
M00040349D:D07	ES 165
M00040351A:C08	ES 165
M00040351D:G07	ES 165
M00040366B:H10	ES 165
M00040367A:C08	ES 165
M00040381A:B06	ES 165
M00040384B:E04	ES 165
M00040391A:G05	ES 165
M00042525B:H01	ES 165
M00042528C:H01	ES 165
M00042554A:D01	ES 165
M00042557D:B06	ES 165
M00042560C:G06	ES 165
M00042579A:D09	ES 165
M00042719A:G08	ES 165
M00042722C:C09	ES 165
M00042724A:G06	ES 165
M00042732B:H06	ES 165
M00042734A:F05	ES 165
M00042742B:E04	ES 165
M00042743D:G10	ES 165
M00042891C:G08	ES 165
M00042894C:A11	ES 165

Clone Name	Tube
M00042908A:F09	ES 165
M00042915B:G11	ES 165
M00054793B:A06	ES 165
M00054911D:E06	ES 166
M00055430A:A01	ES 166
M00055433D:G03	ES 166
M00055448B:E05	ES 166
M00055454A:D02	ES 166
M00055456C:H06	ES 166
M00055466A:F06	ES 166
M00055468A:A08	ES 166
M00055527B:E01	ES 166
M00055639A:E06	ES 166
M00055653C:B07	ES 166
M00055676A:G02	ES 166
M00055724B:E04	ES 166
M00055724D:C07	ES 166
M00055725D:D09	ES 166
M00055735A:H08	ES 166
M00055745B:A08	ES 166
M00055757A:B01	ES 166
M00055794A:E10	ES 166
M00055805A:H02	ES 166
M00055809A:B09	ES 166
M00055810C:D03	ES 166
M00055818B:D01	ES 166
M00055873D:C02	ES 166
M00055880B:H10	ES 166
M00055919B:C10	ES 166
M00055925D:B07	ES 166
M00055961C:B10	ES 166
M00055975B:F09	ES 166
M00055980C:B04	ES 166
M00056004B:C05	ES 166
M00056024B:F09	ES 166
M00056035D:A08	ES 166
M00056057C:F06	ES 166
M00056105A:D06	ES 166
M00056133A:E11	ES 166
M00056215D:F02	ES 166
M00056217D:E10	ES 166
M00056220D:G02	ES 166
M00056230D:E07	ES 166
M00056244A:B06	ES 166
M00056244C:H05	ES 166

Clone Name	Tube
M00056304A:H05	ES 166
M00056320B:A03	ES 166
M00056342A:C03	ES 166
M00056345D:A04	ES 166
M00056436C:F01	ES 166
M00056458C:E01	ES 166
M00042350A:A05	ES 166
M00042433A:E11	ES 166
M00042462B:C02	ES 166
M00042512D:D10	ES 166
M00042766C:D05	ES 166
M00042788A:F04	ES 166
M00042794A:F01	ES 166
M00042796A:A10	ES 166
M00042801C:D01	ES 166
M00042822A:H04	ES 166
M00042857C:E01	ES 166
M00042858C:G11	ES 166
M00042860B:C07	ES 166
M00042863D:F09	ES 166
M00042878D:F05	ES 166
M00042878D:G06	ES 166
M00042352B:A04	ES 166
M00042352D:B03	ES 166
M00042449B:F05	ES 166
M00042457C:B06	ES 166
M00042516B:D01	ES 166
M00042520B:H04	ES 166
M00043299A:B10	ES 166
M00043306D:C01	ES 166
M00043313D:E09	ES 166
M00043328C:E04	ES 166
M00043336D:B03	ES 166
M00043339C:F11	ES 166
M00043355A:D07	ES 166
M00043358C:A02	ES 166
M00043402B:G07	ES 166
M00054499A:C08	ES 166
M00054528B:E05	ES 166
M00054536B:B01	ES 166
M00054538D:C12	ES 166
M00054542B:A10	ES 166
M00054548C:H06	ES 166
M00054569A:B07	ES 166
M00054579A:C02	ES 166

CloneName	Tube
M00054599D:B03	ES 166
M00054623C:F05	ES 166
M00054643D:F07	ES 166
M00054675D:G03	ES 166
M00054682B:H02	ES 166
M00054683D:G11	ES 166
M00054686A:A09	ES 166
M00054686A:F10	ES 166
M00054693A:E11	ES 166
M00054708C:B06	ES 167
M00054714B:G10	ES 167
M00054725C:D09	ES 167
M00054744C:F12	ES 167
M00054781B:H04	ES 167
M00054781D:A11	ES 167
M00054786C:D08	ES 167
M00054807D:C11	ES 167
M00054817D:A11	ES 167
M00054818B:F10	ES 167
M00054843A:C01	ES 167
M00054856C:D03	ES 167
M00054866B:C08	ES 167
M00054890C:D05	ES 167
M00054908C:A01	ES 167
M00054931D:E10	ES 167
M00054973B:E12	ES 167
M00054978C:F01	ES 167
M00055001C:G10	ES 167
M00055002B:E08	ES 167
M00055004C:H05	ES 167
M00055023A:E11	ES 167
M00055043B:H08	ES 167
M00055055C:F01	ES 167
M00055081A:A05	ES 167
M00055093B:A03	ES 167
M00055108B:A02	ES 167
M00055117A:E02	ES 167
M00055166C:D10	ES 167
M00055221C:H11	ES 167
M00055232A:E08	ES 167
M00055239D:F11	ES 167
M00055240A:A08	ES 167
M00055244B:F07	ES 167
M00055254A:H03	ES 167
M00055337B:C04	ES 167

Clone Name	Tube
M00055375C:F12	ES 167
M00055387C:C12	ES 167
M00055391B:C07	ES 167
M00055395D:D11	ES 167
M00055402A:H01	ES 167
M00055420A:E06	ES 167
M00055423A:B08	ES 167
M00055423C:G12	ES 167
M00055423C:H10	ES 167
M00055424B:H06	ES 167
M00055424D:G05	ES 167
M00055425C:A04	ES 167
M00055473C:F02	ES 167
M00055477D:B01	ES 167
M00042585A:H11	ES 167
M00042585D:D03	ES 167
M00042585D:E10	ES 167
M00042586A:B01	ES 167
M00042588C:E02	ES 167
M00042621C:C04	ES 167
M00042951D:G12	ES 167
M00042960B:C06	ES 167
M00042967D:C01	ES 167
M00042970C:B01	ES 167
M00042972C:F04	ES 167
M00042976D:C01	ES 167
M00042982D:A10	ES 167
M00042986D:E03	ES 167
M00042996B:H08	ES 167
M00043013B:E03	ES 167
M00043015D:D05	ES 167
M00043016B:F09	ES 167
M00043017C:D08	ES 167
M00043063C:H05	ES 167
M00043070A:C03	ES 167
M00043113C:G09	ES 167
M00042617B:E01	ES 167
M00043074C:D07	ES 167
M00043076D:A02	ES 167
M00043077B:F11	ES 167
M00043077C:D12	ES 167
M00043077C:G10	ES 167
M00043099A:H04	ES 167
M00043101D:G11	ES 167
M00043134A:F05	ES 167

Clone Name	Tube
M00043152C:B10	ES 167
M00043213A:D05	ES 167
M00043219C:C02	ES 167
M00043221D:C12	ES 167
M00043222C:B06	ES 167
M00043455B:C08	ES 167
M00043465C:H11	ES 167
M00043470A:C10	ES 167
M00043485C:C03	ES 167
M00043490C:F02	ES 167
M00043495C:H05	ES 167
M00043528A:E11	ES 167
M00043529A:B08	ES 167
M00043640A:B01	ES 167

Example 68: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

cDNA libraries were constructed from mRNA isolated from the cell lines indicated in Table 109. The specific library from which any polynucleotide was isolated is indicated in Table 106, with the number of the entry under the "LIBRARY" column correlating to the library number in Table 109. Polynucleotides expressed by the selected cell lines were isolated and analyzed; the sequences of these polynucleotides were about 275-300 nucleotides in length.

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were

discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

5 The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 2396 sequences listed as SEQ ID NOS: 13271-15666 in the accompanying Sequence Listing and summarized in Table 106. Each identified polynucleotide represents sequence
10 from at least a partial mRNA transcript.

Table 106 provides: 1) the SEQ ID NO assigned to each sequence for use in the present specification; 2) the cluster to which the sequence is assigned; 3) the sequence name used as an internal identifier of the sequence; 4) the orientation of the insert in the clone (F=forward; R=reverse); 5) the name assigned to the clone from which the sequence
15 was isolated; and 6) the library from which the sequence was originally isolated. Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length
20 mRNA or gene.

Example 69: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:13271-15666 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to
25 search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs (National Center for Biotechnology Information, Bethesda, Maryland; see also Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences
30 or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 68.

Tables 107A and 107B (inserted before the claims) provide the alignment summaries having a p value of 1×10^{-2} or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Table 107A

provides the SEQ ID NO of the query sequence, the accession number of the GenBank database entry of the homologous sequence, and the p value of the alignment. Table 107B provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous sequence, and the p value of the alignment. The alignments provided in Tables 107A and 107B are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification. The activity of the polypeptide encoded by the SEQ ID NOS listed in Tables 107A and 107B can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and actual activities and functions of the nearest neighbor sequences listed in Table 107B and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the corresponding polynucleotides.

Example 70: Members of Protein Families

SEQ ID NOS: 13271-15666 were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table provides the SEQ ID NO: of the query sequence, the profile name, and a brief description of the profile hit.

Table 108		
SEQ ID	Profilename	Description
13680	ATPases	ATPases Associated with Various Cellular Activities
13807	ATPases	ATPases Associated with Various Cellular Activities

Table 108		
SEQ ID	Profilename	Description
13809	ATPases	ATPases Associated with Various Cellular Activities
13810	ATPases	ATPases Associated with Various Cellular Activities
13932	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
13953	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
13977	dualspecphosphatase	Dual specificity phosphatase, catalytic domain
13978	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
13989	EFhand	EF-hand
14008	ATPases	ATPases Associated with Various Cellular Activities
14049	Zincfing_C2H2	Zinc finger, C2H2 type
14051	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
14053	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
14380	WD_domain	WD domain, G-beta repeats
14685	Dead_box_helic	DEAD and DEAH box helicases
14803	C2	C2 domain (prot. kinase C like)
14903	dualspecphosphatase	Dual specificity phosphatase, catalytic domain
14907	Dead_box_helic	DEAD and DEAH box helicases
14908	Dead_box_helic	DEAD and DEAH box helicases
15014	WD_domain	WD domain, G-beta repeats
15029	BZIP	Basic region plus leucine zipper transcription factors
15263	WD_domain	WD domain, G-beta repeats
15353	WD_domain	WD domain, G-beta repeats
15479	ATPases	ATPases Associated with Various Cellular Activities
15498	ras	Ras family
15557	ras	Ras family
15570	neur_chan	Neurotransmitter-gated ion-channel
15572	tor_domain2	kinase domain of tors (Christoph Reinhard)
15576	homeobox	Homeobox Domain
15588	Metallothion	Metallothioneins
15597	asp	Eukaryotic aspartyl proteases

Some polynucleotides exhibited multiple profile hits where the query sequence contains overlapping profile regions, and/or where the sequence contains two different functional domains. Each of the profile hits of Table 108 are described in more detail below. The acronyms for the profiles (provided in parentheses) are those used to identify the profile in the Pfam and Prosite databases. The Pfam database can be accessed through

web sites supported by the Washington University, St. Louis (Missouri), The Sanger Centre (United Kingdom); and The Karolinska Institute Center for Genomics Research. The Prosite database is publically available through the ExPASy Molecular Biology Server. The public information available on the Pfam and Prosite databases regarding the various profiles, including but not limited to the activities, function, and consensus sequences of various proteins families and protein domains, is incorporated herein by reference.

Eukaryotic Aspartyl Proteases (asp; Pfam Accession No. PF00026). One SEQ ID NO corresponds to a gene encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) 17:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) 19:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) 30:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains.

ATPases Associated with Various Cellular Activities (ATPases; Pfam Accession No. PF0004). Some SEQ ID NOS correspond to a sequence that encodes a member of a family of ATPases Associated with diverse cellular Activities (AAA). The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids containing an ATP-binding site (Froehlich *et al.*, *J. Cell Biol.* (1991) 114:443; Erdmann *et al.*, *Cell* (1991) 64:499; Peters *et al.*, *EMBO J.* (1990) 9:1757; Kunau *et al.*, *Biochimie* (1993) 75:209-224; Confalonieri *et al.*, *BioEssays* (1995) 17:639; see also the AAA Server Homepage). The AAA domain, which can be present in one or two copies, acts as an ATP-dependent protein clamp (Confalonieri *et al.* (1995) *BioEssays* 17:639) and contains a highly conserved region located in the central part of the domain.

Basic Region Plus Leucine Zipper Transcription Factors (BZIP; Pfam Accession No. PF00170). One SEQ ID NO represents a polynucleotide encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization.

C2 domain (C2; Pfam Accession No. PF00168). One SEQ ID NO corresponds to a sequence encoding a C2 domain, which is involved in calcium-dependent phospholipid binding (Davletov *J. Biol. Chem.* (1993) 268:26386-26390) or, in proteins that do not bind calcium, the domain may facilitate binding to inositol-1,3,4,5-tetraphosphate (Fukuda *et al.*

J. Biol. Chem. (1994) 269:29206-29211; Sutton et al. *Cell* (1995) 80:929-938).

DEAD and DEAH box families ATP-dependent helicases (Dead box helic; Pfam Accession No. PF00270). Some SEQ ID NOS represent polynucleotides encoding a novel member of the DEAD and DEAH box families (Schmid et al., *Mol. Microbiol.* (1992) 6:283; Linder et al., *Nature* (1989) 337:121; Wassarman, et al., *Nature* (1991) 349:463). All members of these families are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members share a number of conserved sequence motifs, some of which are specific to the DEAD family, with others shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman *Nature* (1988) 333:22 and *Nature* (1988) 333:578 (Errata)). One of these motifs, called the 'D-E-A-D-box', represents a special version of the B motif of ATP-binding proteins. Proteins that have His instead of the second Asp and are 'D-E-A-H-box' proteins (Wassarman et al., *Nature* (1991) 349:463; Harosh, et al., *Nucleic Acids Res.* (1991) 19:6331; Koonin, et al., *J. Gen. Virol.* (1992) 73:989).

Dual specificity phosphatase (DSPc; Pfam Accession No. PF00782). Some SEQ ID NOS correspond to sequences that encode members of a family of dual specificity phosphatases (DSPs). DSPs are Ser/Thr and Tyr protein phosphatases that comprise a tertiary fold highly similar to that of tyrosine-specific phosphatases, except for a "recognition" region connecting helix alpha1 to strand beta1. This tertiary fold may determine differences in substrate specific between VH-1 related dual specificity phosphatase (VHR), the protein tyrosine phosphatases (PTPs), and other DSPs. Phosphatases are important in the control of cell growth, proliferation, differentiation and transformation.

EF Hand (Efhand; Pfam Accession No. PF00036). One SEQ ID NO corresponds to a polynucleotide encoding a member of the EF-hand protein family, a calcium binding domain shared by many calcium-binding proteins belonging to the same evolutionary family (Kawasaki et al., *Protein. Prof.* (1995) 2:305-490). The domain is a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain, with a calcium ion coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand).

Homeobox domain (homeobox; Pfam Accession No. PF00046). One SEQ ID NO represents a polynucleotide encoding a protein having a homeobox domain. The

'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) 17:277-280; Gehring *et al Annu. Rev. Genet.* (1986) 20:147-173; Schofield *Trends Neurosci.* (1987) 10:3-6) first identified in number of *Drosophila* homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

```

15      xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxHHHHHHHHttHHHHHHHHHxxxxxxxxxxxx
      1                                                                                      60

```

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain.

Metallothioneins (metalthio; Pfam Accession No. PF00131). One SEQ ID NO corresponds to a polynucleotide encoding a member of the metallothionein (MT) protein family (Hamer *Annu. Rev. Biochem.* (1986) 55:913-951; and Kagi *et al. Biochemistry* (1988) 27:8509-8515), small proteins which bind heavy metals such as zinc, copper, cadmium, nickel, *etc.*, through clusters of thiolate bonds. MT's occur throughout the animal kingdom and are also found in higher plants, fungi and some prokaryotes. On the basis of structural relationships MT's have been subdivided into three classes. Class I includes mammalian MT's as well as MT's from crustacean and molluscs, but with clearly related primary structure. Class II groups together MT's from various species such as sea urchins, fungi, insects and cyanobacteria which display none or only very distant correspondence to class I MT's. Class III MT's are atypical polypeptides containing gamma-glutamylcysteinyl units.

Neurotransmitter-Gated Ion-Channel (neur_chan; Pfam Accession No. PF00065). One SEQ ID NO corresponds to a sequence encoding a neurotransmitter-gated ion channel. Neurotransmitter-gated ion-channels, which provide the molecular basis for rapid signal transmission at chemical synapses, are post-synaptic oligomeric transmembrane complexes

that transiently form a ionic channel upon the binding of a specific neurotransmitter. Five types of neurotransmitter-gated receptors are known: 1) nicotinic acetylcholine receptor (AChR); 2) glycine receptor; 3) gamma-aminobutyric-acid (GABA) receptor; 4) serotonin 5HT3 receptor; and 5) glutamate receptor. All known sequences of subunits from neurotransmitter-gated ion-channels are structurally related, and are composed of a large extracellular glycosylated N-terminal ligand-binding domain, followed by three hydrophobic transmembrane regions that form the ionic channel, followed by an intracellular region of variable length. A fourth hydrophobic region is found at the C-terminal of the sequence.

10 Ras family proteins (ras; Pfam Accession No. PF00071). Some SEQ ID NOS represent polynucleotides encoding the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, *Biochemistry* 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg²⁺ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, *Biochemistry* 30:4637-4648.

20 RNA Recognition Motif (rrm; Pfam Accession No. PF00076). Some SEQ ID NOS correspond to sequence encoding an RNA recognition motif, also known as an RRM, RBD, or RNP domain. This domain, which is about 90 amino acids long, is contained in eukaryotic proteins that bind single-stranded RNA (Bandziulis et al. *Genes Dev.* (1989) 3:431-437; Dreyfuss et al. *Trends Biochem. Sci.* (1988) 13:86-91). Two regions within the RNA-binding domain are highly conserved: the first is a hydrophobic segment of six residues (which is called the RNP-2 motif), the second is an octapeptide motif (which is called RNP-1 or RNP-CS).

30 Kinase Domain of Tors (tor_domain2). One SEQ ID NO corresponds to a member of the TOR lipid kinase protein family. This family is composed of large proteins with a lipid and protein kinase domain and characterized through their sensitivity to rapamycin (an antifungal compound). TOR proteins are involved in signal transduction downstream of PI3 kinase and many other signals. TOR (also called FRAP, RAFT) plays a role in regulating protein synthesis and cell growth., and in yeast controls translation initiation and

early G1 progression. See, e.g., Barbet *et al. Mol Biol Cell.* (1996) 7(1):25-42; Helliwell *et al. Genetics* (1998) 148:99-112.

WD Domain, G-Beta Repeats (WD domain; Pfam Accession No. PF00400). Some SEQ ID NOS represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat).

Zinc Finger, C2H2 Type (Zincfing C2H2; Pfam Accession No. PF00096). One SEQ ID NO corresponds to a polynucleotide encoding a member of the C2H2 type zinc finger protein family, which contain zinc finger domains that facilitate nucleic acid binding (Klug *et al., Trends Biochem. Sci.* (1987) 12:464; Evans *et al., Cell* (1988) 52:1; Payre *et al., FEBS Lett.* (1988) 234:245; Miller *et al., EMBO J.* (1985) 4:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99).

In addition to the conserved zinc ligand residues, a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al., J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position, which is generally an aromatic or aliphatic residue, is located four residues after the second cysteine.

25

Example 71: Differential Expression of Polynucleotides of the Invention: Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 109 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, and the approximate number of clones in the library.

30

Table 109. Description of cDNA Libraries

Library (Lib#)	Description	Number of Clones in Library
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMVEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMVEC) - bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMVEC) - VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349

- The KM12L4 cell line (Morikawa, et al., *Cancer Research* (1988) 48:6863) is derived from the KM12C cell line (Morikawa et al. *Cancer Res.* (1988) 48:1943-1948),.
- 5 The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B₂ surgical specimen (Morikawa *et al.* *Cancer Res.* (1988) 48:6863). The KM12L4-A is a highly metastatic subline derived from KM12C (Yeatman *et al.* *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling *et al.* *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4,
- 10 KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa *et al.*, *supra*; Radinsky *et al.* *Clin. Cancer Res.* (1995) 1:19;

Yeatman *et al.*, (1995) *supra*; Yeatman *et al. Clin. Exp. Metastasis* (1996) 14:246). The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MDA-MB-231 and MCF-7 cell lines are well-recognized in the art as a models for the study of human breast cancer (see, *e.g.*, Chandrasekaran *et al.*, *Cancer Res.* (1979) 39:870; Gastpar *et al.*, *J Med Chem* (1998) 41:4965; Ranson *et al.*, *Br J Cancer* (1998) 77:1586; and Kuang *et al.*, *Nucleic Acids Res* (1998) 26:1116).

The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human lung cancer (see, *e.g.*, Varki *et al.*, *Int J Cancer* (1987) 40:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) 10:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) 15:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cell lines were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will

have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Example 72: Differential Expression of Genes Corresponding to Polynucleotides of the Invention

A number of polynucleotide sequences have been identified that are differentially
 5 expressed between, for example, cells derived from high metastatic potential cancer tissue
 and low metastatic cancer cells, and between cells derived from metastatic cancer tissue
 and normal tissue. Evaluation of the levels of expression of the genes corresponding to
 these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate
 rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes
 10 corresponding to differentially expressed sequences described herein can be therapeutic
 targets due to their involvement in regulation (*e.g.*, inhibition or promotion) of
 development of, for example, the metastatic phenotype. For example, sequences that
 correspond to genes that are increased in expression in high metastatic potential cells
 relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences
 15 involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

Detection of the relative expression levels of differentially expressed
 polynucleotides described herein can provide valuable information to guide the clinician in
 the choice of therapy. For example, a patient sample exhibiting an expression level of one
 or more of these polynucleotides that corresponds to a gene that is increased in expression
 20 in metastatic or high metastatic potential cells may warrant more aggressive treatment for
 the patient. In contrast, detection of expression levels of a polynucleotide sequence that
 corresponds to expression levels associated with that of low metastatic potential cells may
 warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of the polynucleotides described herein can thus be used
 25 as, for example, diagnostic markers, prognostic markers, for risk assessment, patient
 treatment and the like. These polynucleotide sequences can also be used in combination
 with other known molecular and/or biochemical markers. The following examples provide
 relative expression levels of polynucleotides from specified cell lines and patient tissue
 samples.

30 The differential expression data for polynucleotides of the invention that have been
 identified as being differentially expressed across various combinations of the libraries
 described above is summarized in Table 110 (inserted prior to the claims). Table 110
 provides: 1) the Sequence Identification Number ("SEQ") assigned to the polynucleotide;
 2) the cluster ("CLST") to which the polynucleotide has been assigned as described above;

3) the library comparisons that resulted in identification of the polynucleotide as being differentially expressed ("Library Pair A,B"), with shorthand names of the compared libraries provided in parentheses following the library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("B"); 6) the "A/B" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "B/A" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

10

Example 73: Source of Biological Materials for Microarray-Based Experiments

The biological materials used in the experiments described in the subsequent examples relating to microarray data are described below.

Source of patient tissue samples

15

Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001). Table 114 provides information about each patient from which the samples were isolated, including: the Patient ID and Path ReportID, numbers assigned to the patient and the pathology reports for identification purposes; the anatomical location of the tumor (AnatomicalLoc); The Primary Tumor Size; the Primary Tumor Grade; the Histopathologic Grade; a description of local sites to which the tumor had invaded (Local Invasion); the presence of lymph node metastases (Lymph Node Metastasis); incidence of lymph node metastases (provided as number of lymph nodes positive for metastasis over the number of lymph nodes examined) (Incidence Lymphnode Metastasis); the Regional Lymphnode Grade; the identification or detection of metastases to sites distant to the tumor and their location (Distant Met & Loc); a description of the distant metastases (Description Distant Met); the grade of distant metastasis (Distant Met Grade); and general comments about the patient or the tumor (Comments). Adenoma was not described in any of the patients. ; adenoma dysplasia (described as hyperplasia by the pathologist) was described in Patient ID No. 695. Extranodal extensions were described in two patients, Patient ID Nos. 784 and 791. Lymphovascular invasion was described in seven patients, Patient ID

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Nos. 128, 278, 517, 534, 784, 786, and 791.. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Polynucleotides on arrays

Polynucleotides spotted on the arrays were generated by PCR amplification of clones derived from cDNA libraries. The clones used for amplification were either the clones from which the sequences described herein (SEQ ID NOS: 13271-15666) were derived, or are clones having inserts with significant polynucleotide sequence overlap with the sequences described herein (SEQ ID NO: 13271-15666) as determined by BLAST2 homology searching.

Example 74: Microarray Design

Each array used in the examples below had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides.

The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

Example 75: Identification Of Differentially Expressed Genes

cDNA probes were prepared from total RNA isolated from the patient cells described in Example 6. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, e.g., Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then

converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling. Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red).

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level of fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final

determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

Tables 115-119 summarizes the results of the differential expression analysis, where the difference in the expression level in the colon tumor cell relative to the matched normal colon cells is greater than or equal to 2 fold (" $\geq 2x$ "), 2.5 fold (" $\geq 2.5x$ "), or 5 fold (" $\geq 5x$ ") in at least 20% or more of the patients analyzed. Each table provides: the SEQ ID NO; the percentage of patients tested having a colon tumor that exhibited at least 2 fold (" $\geq 2x$ "), 2.5 fold (" $\geq 2.5x$ "), or 5 fold (" $\geq 5x$ ") increase in expression levels of the indicated gene relative to matched normal colon tissue; and the ratio data for each patient sample tested (columns headed by "P#", indicating the Patient Identification Number, e.g., "P15" indicates the ratio data for patient 15).

Table 115

SEQ ID NO	%Pts $\geq 2x$ T/N	% Pts $\geq 2.5x$ T/N	% Pts $\geq 5x$ T/N	P15	P52	P121	P125
13288	30.3	15.2	3.0	1.855	2.705	1.000	2.280
13292	45.5	39.4	18.2	2.196	1.719	0.604	2.388
13397	27.3	18.2	6.1	1.000	1.620	1.822	1.692
13409	21.2	18.2	15.2	1000.000	0.001	2.345	1.000

13418	27.3	18.2	6.1	1.000	1.620	1.822	1.692
13425	45.5	12.1	3.0	1.870	3.104	1.361	2.388
13516	42.4	9.1	0.0	2.211	2.347	1.000	1.493
13542	48.5	27.3	12.1	1.735	3.110	1.379	2.277
13543	21.2	18.2	18.2	1.000	1.000	0.330	1.349
13549	24.2	12.1	0.0	1.614	2.348	1.498	1.916
13568	21.2	18.2	18.2	1.000	1.000	0.330	1.349
13599	21.2	9.1	6.1	1.000	1.000	2.211	1.182
13623	45.5	12.1	3.0	1.870	3.104	1.361	2.388
13624	48.5	30.3	3.0	1.000	1.592	2.248	2.315
13651	27.3	18.2	6.1	1.000	1.620	1.822	1.692
13659	21.2	9.1	6.1	1.000	1.000	2.211	1.182
13675	21.2	9.1	3.0	1.000	2.366	1.546	1.562
13676	21.2	9.1	3.0	1.000	2.366	1.546	1.562
13682	36.4	18.2	0.0	2.584	1.332	1.952	1.641
13691	51.5	24.2	3.0	2.481	2.253	2.234	1.431
13735	21.2	18.2	15.2	1000.000	0.001	2.345	1.000
13804	21.2	9.1	3.0	1.000	2.366	1.546	1.562
13808	42.4	15.2	0.0	1.489	2.019	3.022	1.121
13835	45.5	12.1	3.0	1.870	3.104	1.361	2.388
13927	45.5	30.3	3.0	1.512	2.748	0.784	2.162
13940	24.2	6.1	0.0	1.190	1.000	0.656	1.456
14009	21.2	12.1	0.0	1.936	1.830	0.831	1.347
14011	48.5	18.2	0.0	2.750	2.458	1.485	1.151
14014	48.5	21.2	0.0	2.069	3.002	1.229	1.631
14025	30.3	18.2	3.0	1.000	1.414	1.236	1.738
14027	21.2	15.2	6.1	1.000	0.839	2.032	2.557
14080	30.3	18.2	3.0	1.000	1.414	1.236	1.738
14081	30.3	18.2	3.0	1.000	1.414	1.236	1.738
14115	30.3	15.2	9.1	1.000	0.271	0.860	1.310
14131	24.2	21.2	15.2	1000.000	1000.000	1.000	1.320
14185	30.3	15.2	3.0	1.855	2.705	1.000	2.280
14224	24.2	21.2	15.2	1000.000	1000.000	1.000	1.320
14225	39.4	21.2	3.0	1.612	2.281	0.785	2.045
14261	39.4	21.2	3.0	1.612	2.281	0.785	2.045

14305	24.2	6.1	0.0	1.190	1.000	0.656	1.456
14319	21.2	12.1	0.0	1.936	1.830	0.831	1.347
14320	39.4	21.2	3.0	1.612	2.281	0.785	2.045
14505	45.5	12.1	3.0	1.870	3.104	1.361	2.388
14562	21.2	3.0	0.0	1.558	2.014	2.250	1.643
14583	24.2	6.1	0.0	1.190	1.000	0.656	1.456
14601	27.3	9.1	3.0	1.327	3.749	1.000	2.045
14604	48.5	30.3	3.0	1.000	1.592	2.248	2.315
14688	30.3	15.2	3.0	1.855	2.705	1.000	2.280
14689	45.5	12.1	3.0	1.870	3.104	1.361	2.388
14690	39.4	18.2	3.0	1.759	1.566	1.000	2.302
14747	39.4	18.2	3.0	1.759	1.566	1.000	2.302
14824	33.3	15.2	0.0	1.829	1.622	1.882	1.957
14849	42.4	9.1	0.0	2.211	2.347	1.000	1.493
14870	45.5	12.1	3.0	1.870	3.104	1.361	2.388
14909	48.5	27.3	12.1	1.735	3.110	1.379	2.277
14927	42.4	24.2	0.0	1.000	1.908	2.267	1.188
14949	33.3	15.2	0.0	1.829	1.622	1.882	1.957
15014	42.4	15.2	3.0	2.059	2.753	1.679	1.587
15117	78.8	63.6	9.1	2.625	4.493	1.642	2.743
15147	45.5	12.1	3.0	1.870	3.104	1.361	2.388
15150	66.7	48.5	6.1	1.000	4.075	1.754	2.436
15159	45.5	12.1	3.0	1.870	3.104	1.361	2.388
15279	30.3	15.2	3.0	1.855	2.705	1.000	2.280
15293	30.3	18.2	0.0	1.285	2.400	0.767	1.270
15299	42.4	9.1	0.0	2.211	2.347	1.000	1.493
15341	24.2	6.1	0.0	1.190	1.000	0.656	1.456
15347	24.2	6.1	0.0	1.190	1.000	0.656	1.456
15373	27.3	21.2	0.0	3.505	0.793	0.809	1.348
15379	24.2	6.1	0.0	1.190	1.000	0.656	1.456
15408	33.3	21.2	9.1	1.000	0.296	3.016	0.794
15413	60.6	48.5	12.1	6.263	1.000	1.832	1.937
15453	63.6	45.5	12.1	1.945	2.010	0.547	3.325
15455	30.3	18.2	3.0	1.000	1.414	1.236	1.738
15460	24.2	6.1	0.0	1.190	1.000	0.656	1.456

15470	45.5	12.1	3.0	1.870	3.104	1.361	2.388
15476	60.6	27.3	3.0	2.256	2.228	1.673	1.937
15490	33.3	24.2	3.0	2.591	0.483	2.580	1.440
15494	48.5	36.4	3.0	1.602	3.209	1.000	2.942
15519	45.5	12.1	3.0	1.870	3.104	1.361	2.388
15525	24.2	3.0	0.0	1.985	2.261	1.000	0.904
15535	54.5	42.4	6.1	1.886	1.000	1.503	3.375
15537	84.8	57.6	18.2	2.529	3.042	2.471	1.669
15551	54.5	36.4	3.0	2.008	0.686	3.104	1.362
15564	30.3	15.2	3.0	1.855	2.705	1.000	2.280
15570	30.3	15.2	3.0	1.855	2.705	1.000	2.280
15577	42.4	9.1	0.0	2.211	2.347	1.000	1.493
15579	42.4	21.2	9.1	2.497	1.837	3.249	1.497
15583	57.6	48.5	9.1	2.603	2.642	1.000	1.939
15584	48.5	27.3	12.1	1.735	3.110	1.379	2.277
15586	42.4	9.1	0.0	2.211	2.347	1.000	1.493
15597	39.4	24.2	3.0	2.006	1.692	1.778	1.662
15618	72.7	45.5	0.0	2.961	3.152	2.712	1.346

Table 116

SEQ ID NO	P128	P130	P133	P141	P156	P228	P264	P266
13288	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
13292	1.594	6.800	1.340	1.131	1.000	2.647	1.628	1.190
13397	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
13409	1000.000	1.000	1000.000	0.482	2.846	0.767	1.631	1.000
13418	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
13425	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
13516	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
13542	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
13543	1000.000	1000.000	1.000	1.000	0.566	1.554	1.000	1.000
13549	1.202	1.852	2.370	1.000	1.000	1.114	1.399	1.239
13568	1000.000	1000.000	1.000	1.000	0.566	1.554	1.000	1.000
13599	3.234	0.001	1.000	8.480	2.077	1.000	0.001	1.445
13623	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357

13624	1.664	1.987	2.307	2.728	1.000	1.239	1.469	2.059
13651	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
13659	3.234	0.001	1.000	8.480	2.077	1.000	0.001	1.445
13675	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
13676	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
13682	1.831	1.503	2.326	1.130	1.773	1.379	2.318	2.019
13691	2.209	1.889	3.114	1.776	1.788	1.879	2.666	2.257
13735	1000.000	1.000	1000.000	0.482	2.846	0.767	1.631	1.000
13804	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
13808	1.559	1.000	1.740	3.133	2.186	1.869	2.023	2.483
13835	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
13927	1.524	1.770	2.846	1.185	1.000	1.460	1.831	2.261
13940	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
14009	0.845	1.286	1.872	1.000	1.000	1.295	1.722	1.785
14011	1.819	1.801	3.227	1.457	2.960	1.388	2.086	2.410
14014	2.515	1.605	2.399	1.803	2.524	1.551	2.284	1.574
14025	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
14027	0.745	1.332	1000.000	1.000	1.000	1.781	1.515	1.747
14080	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
14081	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
14115	2.331	1.641	1000.000	1.252	1.000	0.595	1.950	0.616
14131	2.888	1.000	0.001	1.000	1.694	0.001	1000.000	1.423
14185	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
14224	2.888	1.000	0.001	1.000	1.694	0.001	1000.000	1.423
14225	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
14261	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
14305	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
14319	0.845	1.286	1.872	1.000	1.000	1.295	1.722	1.785
14320	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
14505	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
14562	1.804	1.641	1.876	1.335	0.766	1.245	1.500	1.000
14583	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
14601	1.427	1.669	1.837	1.265	1.000	1.667	1.000	1.374
14604	1.664	1.987	2.307	2.728	1.000	1.239	1.469	2.059
14688	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236

14689	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
14690	1.518	1.997	2.298	2.273	1.000	1.234	1.186	1.730
14747	1.518	1.997	2.298	2.273	1.000	1.234	1.186	1.730
14824	2.959	1.821	2.234	1.181	1.827	1.000	2.042	1.970
14849	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
14870	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
14909	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
14927	2.160	1.416	1.000	3.531	2.974	1.798	1.899	2.065
14949	2.959	1.821	2.234	1.181	1.827	1.000	2.042	1.970
15014	1.479	1.669	2.442	1.352	1.367	1.605	2.145	2.098
15117	1.839	2.548	2.954	2.234	1.816	1.352	3.390	2.541
15147	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
15150	2.762	2.081	4.111	2.306	2.391	1.675	2.572	3.031
15159	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
15279	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
15293	1.871	1.869	2.588	1.834	1.718	1.197	1.965	2.023
15299	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
15341	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
15347	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
15373	2.297	0.855	1.659	1.607	0.252	1.602	2.866	1.292
15379	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
15408	2.074	1.438	1.552	2.403	0.647	0.605	0.469	0.528
15413	2.828	2.795	2.732	2.548	0.073	1.201	1.722	1.181
15453	1.714	3.061	4.635	1.688	1.230	1.241	1.237	1.852
15455	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
15460	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
15470	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
15476	2.229	2.131	2.194	2.235	2.121	1.388	3.468	2.115
15490	2.650	0.815	1.629	1.586	0.155	1.408	2.830	1.636
15494	1.385	2.044	2.510	0.628	1.763	1.000	1.000	1.687
15519	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
15525	1.454	1.000	1.567	2.350	1.729	2.071	1.439	1.540
15535	2.843	2.931	1.690	1.678	0.724	2.656	2.035	3.526
15537	2.490	1.937	3.729	2.105	2.224	2.547	2.605	4.402
15551	3.412	2.374	1.404	4.761	3.241	2.253	1.384	1.912

15564	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
15570	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
15577	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
15579	1.496	1.483	2.427	1.764	1.000	1.231	1.413	1.000
15583	1.452	1.915	2.252	1.342	2.516	1.278	2.179	4.223
15584	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
15586	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
15597	1.778	1.200	2.169	1.462	1.570	1.784	1.937	2.633
15618	2.064	1.288	2.075	2.527	2.239	1.745	3.772	3.393
15654	2.340	0.001	0.001	2.927	4.830	1.708	1.651	1.586

Table 117

SEQ ID NO	P268	P278	P295	P339	P341	P356	P360	P392
13288	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
13292	1.194	1.000	1.000	1.474	3.006	2.766	1.622	10.061
13397	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
13409	1000.000	1.332	1.000	0.344	1.537	1.000	0.001	0.464
13418	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
13425	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
13516	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
13542	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427
13543	1.000	1000.000	1.000	1.196	2.209	1000.000	0.001	1.000
13549	1.000	1.000	1.000	1.737	2.382	3.061	2.679	1.361
13568	1.000	1000.000	1.000	1.196	2.209	1000.000	0.001	1.000
13599	2.467	2.166	21.707	0.615	1.616	1.000	1.000	1.000
13623	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
13624	2.359	1.552	2.918	1.647	4.706	3.623	1.979	1.677
13651	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
13659	2.467	2.166	21.707	0.615	1.616	1.000	1.000	1.000
13675	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
13676	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
13682	2.677	2.809	2.969	1.373	2.087	3.804	1.612	1.163
13691	2.468	5.262	4.008	1.487	4.366	2.078	1.781	1.332

13735	1000.000	1.332	1.000	0.344	1.537	1.000	0.001	0.464
13804	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
13808	2.565	1.856	1.000	1.000	2.449	1.000	2.097	2.647
13835	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
13927	1.369	1.000	1.000	1.679	3.084	2.855	2.104	0.927
13940	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
14009	1.412	1.431	3.103	1.000	2.847	2.621	1.000	1.117
14011	2.240	2.040	1.000	1.000	2.450	3.440	2.045	1.998
14014	1.837	2.201	2.518	1.604	2.248	2.989	1.570	1.409
14025	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
14027	0.713	1000.000	0.632	2.389	0.202	1.000	1.000	0.356
14080	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
14081	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
14115	2.151	2.384	2.417	0.573	1.451	2.652	1.000	0.734
14131	1.000	1.509	9.879	1000.000	2.327	0.001	1.236	0.870
14185	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
14224	1.000	1.509	9.879	1000.000	2.327	0.001	1.236	0.870
14225	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
14261	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
14305	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
14319	1.412	1.431	3.103	1.000	2.847	2.621	1.000	1.117
14320	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
14505	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
14562	0.718	1.000	1.000	1.675	2.301	1.361	2.161	1.825
14583	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
14601	0.789	1.609	1.000	0.797	1.000	2.075	2.491	2.505
14604	2.359	1.552	2.918	1.647	4.706	3.623	1.979	1.677
14688	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
14689	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
14690	1.864	1.428	2.631	1.854	3.430	3.182	1.892	1.581
14747	1.864	1.428	2.631	1.854	3.430	3.182	1.892	1.581
14824	2.495	2.090	3.320	1.000	3.907	2.976	1.875	1.000
14849	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
14870	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
14909	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427

14927	2.183	2.285	3.554	1.247	2.093	1.840	1.855	1.504
14949	2.495	2.090	3.320	1.000	3.907	2.976	1.875	1.000
15014	2.006	1.696	2.261	1.611	2.154	3.791	1.816	1.356
15117	1.535	2.851	4.154	2.055	6.047	4.103	3.367	2.029
15147	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
15150	2.274	1.266	4.526	2.591	5.409	3.138	2.675	1.391
15159	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
15279	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
15293	1.971	1.699	2.355	1.453	3.122	2.528	1.949	1.326
15299	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
15341	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
15347	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
15373	2.516	0.852	1.775	0.818	4.294	2.281	1.119	0.890
15379	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
15408	1.794	1.486	5.006	0.398	4.768	0.001	2.344	2.434
15413	2.079	1.664	1.000	1.871	2.812	2.693	5.094	1.947
15453	2.325	2.043	2.530	2.411	5.749	5.509	3.490	2.008
15455	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
15460	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
15470	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
15476	1.977	1.676	1.774	1.542	2.538	1.867	2.312	1.000
15490	2.942	0.729	1.772	0.861	15.794	2.349	1.363	0.808
15494	1.457	1.690	2.551	1.860	4.114	3.548	3.125	0.792
15519	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
15525	1.586	1.943	1.000	0.699	1.593	2.039	1.798	0.774
15535	2.157	1.922	3.895	4.143	2.655	1.914	2.159	3.312
15537	3.442	3.933	5.994	1.448	8.695	7.488	2.687	2.449
15551	2.467	1.000	7.584	1.417	3.693	1.947	1.539	4.429
15564	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
15570	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
15577	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
15579	2.485	2.369	1.000	1.820	3.354	5.046	1.820	0.703
15583	3.203	1.593	4.012	1.593	6.374	6.940	3.158	0.947
15584	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427
15586	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623

15597	2.439	1.482	2.156	1.390	3.500	3.654	1.655	0.771
15618	2.448	2.617	4.003	1.289	2.940	3.894	2.277	1.202
15654	2.328	1.359	9.253	0.383	1.835	0.001	1.000	0.714

Table 118

SEQ ID NO	P393	P413	P505	P517	P534	P546	P577	P695
13288	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
13292	14.260	2.516	1.498	3.747	1.300	5.779	11.202	0.001
13397	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
13409	1.000	1.000	0.458	1.249	0.001	1000.000	0.702	1.000
13418	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
13425	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
13516	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
13542	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
13543	1.000	1.000	1000.000	1.477	1.645	1.000	1.389	1.000
13549	0.914	1.603	1.936	1.485	2.430	1.999	1.647	4.375
13568	1.000	1.000	1000.000	1.477	1.645	1.000	1.389	1.000
13599	1.000	1.000	1.436	0.517	1.000	1.469	1.000	1.000
13623	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
13624	1.224	3.432	2.806	1.328	2.470	2.592	1.929	6.973
13651	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
13659	1.000	1.000	1.436	0.517	1.000	1.469	1.000	1.000
13675	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
13676	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
13682	1.258	2.153	1.849	1.445	1.000	1.531	1.637	3.302
13691	1.000	1.327	2.871	1.116	1.903	2.200	2.644	0.001
13735	1.000	1.000	0.458	1.249	0.001	1000.000	0.702	1.000
13804	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
13808	1.560	1.982	2.159	1.278	1.425	1.204	3.046	2.068
13835	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
13927	0.763	1.602	2.797	1.265	2.765	2.236	2.548	5.071
13940	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
14009	2.102	1.689	4.429	0.830	1.000	1.000	2.108	2.208
14011	1.935	1.911	2.812	1.000	1.854	1.793	2.441	0.001

14014	1.320	1.404	1.553	1.000	1.957	1.816	2.156	3.745
14025	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
14027	0.851	0.750	0.815	0.258	0.712	1.229	0.190	1.000
14080	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
14081	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
14115	2.765	1.000	2.202	0.472	0.490	1.417	0.725	0.001
14131	1.000	1.000	1.000	1.000	1.000	1.530	0.769	1.000
14185	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
14224	1.000	1.000	1.000	1.000	1.000	1.530	0.769	1.000
14225	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
14261	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
14305	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
14319	2.102	1.689	4.429	0.830	1.000	1.000	2.108	2.208
14320	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
14505	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
14562	1.000	1.518	1.980	1.518	2.526	1.588	1.865	2.251
14583	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
14601	0.743	2.126	1.613	1.177	2.128	1.000	1.951	6.931
14604	1.224	3.432	2.806	1.328	2.470	2.592	1.929	6.973
14688	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
14689	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
14690	1.205	3.301	2.749	1.256	2.474	2.345	1.826	8.108
14747	1.205	3.301	2.749	1.256	2.474	2.345	1.826	8.108
14824	1.000	1.793	2.719	1.679	1.000	1.549	2.076	0.001
14849	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
14870	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
14909	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
14927	2.809	1.534	1.366	1.197	2.545	1.964	1.506	0.001
14949	1.000	1.793	2.719	1.679	1.000	1.549	2.076	0.001
15014	1.249	2.009	1.832	1.488	1.379	1.975	2.128	13.930
15117	1.781	2.929	2.183	2.759	3.853	3.092	2.051	7.549
15147	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
15150	1.000	3.187	2.564	0.756	1.226	3.841	3.201	16.724
15159	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
15279	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930

15293	1.952	1.472	1.917	1.516	2.305	2.677	2.620	2.660
15299	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
15341	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
15347	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
15373	0.537	1.790	0.727	0.750	0.329	1.100	1.239	0.001
15379	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
15408	0.852	1.789	3.765	0.686	3.176	1.591	1.852	0.001
15413	2.044	17.760	4.034	1.988	0.026	3.908	2.394	42.662
15453	1.088	5.833	3.519	1.572	2.641	4.011	1.695	7.783
15455	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
15460	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
15470	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
15476	1.000	3.033	1.912	1.699	2.147	2.780	2.155	2.518
15490	0.337	2.339	0.768	0.563	0.359	1.242	1.492	1.000
15494	1.000	2.266	2.040	1.000	2.747	2.620	1.718	14.145
15519	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
15525	1.243	1.766	1.547	0.843	1.000	1.498	2.122	4.421
15535	5.268	1.518	2.253	3.678	0.766	1.565	1.000	1.853
15537	0.815	2.497	3.234	2.275	2.344	3.596	5.023	12.124
15551	1.128	0.885	1.237	1.434	3.327	3.206	1.355	0.001
15564	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
15570	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
15577	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
15579	1.240	2.239	2.841	1.000	2.270	2.614	0.583	5.244
15583	0.633	2.821	2.976	1.253	1.675	3.657	2.284	8.587
15584	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
15586	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
15597	1.000	1.801	1.978	1.000	3.188	1.607	2.276	13.068
15618	0.790	3.524	3.377	2.062	2.123	1.959	1.626	1.000
15654	0.001	1.346	1.831	1.000	1.646	1.944	1.549	1.000

Table 119

SEQ ID					
NO	P784	P786	P791	P888	P889
13288	1.000	1.000	4.202	1.464	2.147

13292	1.000	1.276	14.034	4.139	3.640
13397	1.708	2.247	1.000	0.441	0.001
13409	1.391	1.857	1.000	0.402	1.000
13418	1.708	2.247	1.000	0.441	0.001
13425	1.328	1.421	2.456	1.910	2.069
13516	1.243	1.679	2.228	2.333	1.774
13542	0.819	1.632	2.808	5.465	2.307
13543	1000.000	0.758	1.000	1.000	1.000
13549	1.000	1.000	1.834	2.776	1.636
13568	1000.000	0.758	1.000	1.000	1.000
13599	1.000	1.000	1.000	0.642	1.000
13623	1.328	1.421	2.456	1.910	2.069
13624	1.000	1.416	2.862	2.690	1.645
13651	1.708	2.247	1.000	0.441	0.001
13659	1.000	1.000	1.000	0.642	1.000
13675	1.000	1.821	1.628	2.276	2.501
13676	1.000	1.821	1.628	2.276	2.501
13682	1.000	1.888	1.915	2.276	1.481
13691	3.336	1.677	2.208	1.000	1.976
13735	1.391	1.857	1.000	0.402	1.000
13804	1.000	1.821	1.628	2.276	2.501
13808	1.000	1.629	2.152	1.000	1.792
13835	1.328	1.421	2.456	1.910	2.069
13927	1.000	1.997	2.083	3.178	3.444
13940	1.000	1.780	1.000	2.177	2.258
14009	1.356	0.696	1.000	1.000	1.463
14011	2.324	1.000	2.379	1.407	2.833
14014	2.137	1.934	2.482	2.035	3.980
14025	0.796	1.000	1.737	1.000	2.218
14027	2.531	3.138	0.395	1.000	1.000
14080	0.796	1.000	1.737	1.000	2.218
14081	0.796	1.000	1.737	1.000	2.218
14115	1000.000	1.984	1000.000	1.374	1.000
14131	3.031	1.000	1.000	1.000	1.000
14185	1.000	1.000	4.202	1.464	2.147

14224	3.031	1.000	1.000	1.000	1.000
14225	0.876	1.781	2.424	4.143	1.977
14261	0.876	1.781	2.424	4.143	1.977
14305	1.000	1.780	1.000	2.177	2.258
14319	1.356	0.696	1.000	1.000	1.463
14320	0.876	1.781	2.424	4.143	1.977
14505	1.328	1.421	2.456	1.910	2.069
14562	1.000	1.000	1.992	2.144	1.615
14583	1.000	1.780	1.000	2.177	2.258
14601	1.290	1.000	1.000	1.995	2.203
14604	1.000	1.416	2.862	2.690	1.645
14688	1.000	1.000	4.202	1.464	2.147
14689	1.328	1.421	2.456	1.910	2.069
14690	0.816	1.000	2.196	2.446	1.518
14747	0.816	1.000	2.196	2.446	1.518
14824	1.585	1.889	2.178	1.806	1.867
14849	1.243	1.679	2.228	2.333	1.774
14870	1.328	1.421	2.456	1.910	2.069
14909	0.819	1.632	2.808	5.465	2.307
14927	2.810	2.638	1.976	1.491	2.955
14949	1.585	1.889	2.178	1.806	1.867
15014	1.253	1.994	1.874	3.193	2.663
15117	1.559	2.762	5.043	4.135	3.753
15147	1.328	1.421	2.456	1.910	2.069
15150	1.306	1.940	2.293	3.897	1.624
15159	1.328	1.421	2.456	1.910	2.069
15279	1.000	1.000	4.202	1.464	2.147
15293	1.511	1.357	1.632	1.891	1.895
15299	1.243	1.679	2.228	2.333	1.774
15341	1.000	1.780	1.000	2.177	2.258
15347	1.000	1.780	1.000	2.177	2.258
15373	0.573	2.678	1.000	2.507	3.278
15379	1.000	1.780	1.000	2.177	2.258
15408	7.866	1.000	1000.000	1.719	1.000
15413	2.625	2.744	4.155	2.105	4.438

15453	1.000	2.139	3.014	3.159	3.381
15455	0.796	1.000	1.737	1.000	2.218
15460	1.000	1.780	1.000	2.177	2.258
15470	1.328	1.421	2.456	1.910	2.069
15476	1.489	2.750	2.910	5.049	4.006
15490	0.419	3.014	0.575	2.397	3.558
15494	1.000	1.815	2.513	3.487	2.180
15519	1.328	1.421	2.456	1.910	2.069
15525	1.000	1.493	2.186	1.000	2.222
15535	1.267	3.638	1.623	5.889	3.339
15537	1.746	2.363	5.515	2.674	3.637
15551	2.399	3.587	3.625	2.567	2.417
15564	1.000	1.000	4.202	1.464	2.147
15570	1.000	1.000	4.202	1.464	2.147
15577	1.243	1.679	2.228	2.333	1.774
15579	0.397	1.000	1.472	5.315	2.250
15583	1.000	1.939	2.505	4.525	2.674
15584	0.819	1.632	2.808	5.465	2.307
15586	1.243	1.679	2.228	2.333	1.774
15597	1.295	1.658	2.836	2.766	2.873
15618	2.167	2.157	3.410	2.828	3.794
15654	1.352	1.000	2.727	0.583	1.000

In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at least one sample and the ratio value is greater than at least about 1.2 fold, preferably greater than at least about 1.5 fold, more preferably greater than at least about 2 fold, where the ratio value is calculated using the method described above.

A differential expression ratio of 1 indicates that the expression level of the gene in the tumor cell was not statistically different from expression of that gene in normal colon cells of the same patient. A differential expression ratio significantly greater than 1 in cancerous colon cells relative to normal colon cells indicates that the gene is increased in expression in cancerous cells relative to normal cells, indicating that the gene plays a role in the development of the cancerous phenotype, and may be involved in promoting

metastasis of the cell. Detection of gene products from such genes can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target.

Likewise, a differential expression ratio significantly less than 1 in cancerous colon cells relative to normal colon cells indicates that, for example, the gene is involved in suppression of the cancerous phenotype. Increasing activity of the gene product encoded by such a gene, or replacing such activity, can provide the basis for chemotherapy. Such gene can also serve as markers of cancerous cells, *e.g.*, the absence or decreased presence of the gene product in a colon cell relative to a normal colon cell indicates that the cell may be cancerous.

Example 76: Functional Analysis Of Gene Products Differentially Expressed In Cancer In Patients

The gene products of genes differentially expressed in cancerous cells are further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype.

Blocking expression of gene products using antisense

The effect of single genes upon development of cancer is assessed through use of antisense oligonucleotides specific for sequences corresponding to a selected sequence. Antisense oligonucleotides are prepared based upon a selected sequence that corresponds to a gene of interest. The antisense oligonucleotide is introduced into a test cell and the effect upon expression of the corresponding gene, as well as the effect upon a phenotype of interest assessed (*e.g.*, a normal cell is examined for induction of the cancerous phenotype, or a cancerous cell is examined for suppression of a cancerous phenotype (*e.g.*, suppression of metastasis)).

Blocking function of gene products using gene product-specific antibodies and/or small molecule inhibitors

The function of gene products corresponding to genes/clusters identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype. In order to generate antibodies, a clone corresponding to a selected gene product/cluster is selected, and a sequence that represents a partial or complete coding sequence is obtained. The resulting clone is then

expressed, the polypeptide produced isolated, and antibodies generated. The antibodies are then combined with cells and the effect upon tumorigenesis assessed.

Where the gene product of the gene/clusters identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecule that inhibit or enhance function of the corresponding protein or protein family.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information. The following materials were deposited with the American Type Culture Collection (CMCC = Chiron Master Culture Collection).

Table 111. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583

MCF-7	October 9, 1998	CRL-12584	10377
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In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 112 (inserted before the claims) provides the ATCC Accession Nos. and internal references (CMCC Nos.) of the ES deposits, all of which were deposited on or before the filing date of the present application. The names of the clones contained within each of these deposits are provided in Table 113 (inserted before the claims).

Table 112		
ES #	CMCC#	ATCC Deposit#
85	5175	PTA-1313
86	5176	PTA-1314
87	5177	PTA-1315
88	5178	PTA-1316
89	5179	PTA-1317
90	5180	PTA-1318
91	5181	PTA-1319
92	5182	PTA-1320
93	5183	PTA-1321
94	5184	PTA-1322
95	5185	PTA-1323
96	5186	PTA-1324
97	5187	PTA-1325
98	5188	PTA-1326
99	5189	PTA-1327
100	5190	PTA-1328
101	5191	PTA-1329
102	5192	PTA-1330
103	5193	PTA-1331
104	5194	PTA-1332
105	5195	PTA-1333
106	5196	PTA-1334
107	5197	PTA-1335
108	5198	PTA-1336
109	5199	PTA-1372
110	5200	PTA-1373

111	5201	PTA-1374
112	5202	PTA-1375
113	5203	PTA-1376
114	5204	PTA-1377
115	5205	PTA-1378
116	5206	PTA-1379
117	5207	PTA-1380
118	5208	PTA-1381
122	5212	PTA-1382
123	5213	PTA-1383
124	5214	PTA-1384
125	5215	PTA-1385
126	5216	PTA-1386
127	5217	PTA-1387
128	5218	PTA-1388
129	5219	PTA-1389
130	5220	PTA-1390
131	5221	PTA-1391
132	5222	PTA-1392
133	5223	PTA-1393
134	5209	PTA-1431
135	5210	PTA-1432
136	5238	PTA-1497

Table 113

Table 113			
ES No.	Clone Name	ES No.	Clone Name
ES 85	M00057077B:D02	ES 109	M00027658B:G03
ES 85	M00057078D:C12	ES 109	M00027660C:E03
ES 85	M00057079D:E09	ES 109	M00027660C:E03
ES 85	M00057080C:C02	ES 109	M00027665B:D01
ES 85	M00057085A:A03	ES 109	M00027681D:D02
ES 85	M00057088B:C02	ES 109	M00027699D:D02
ES 85	M00057091A:C03	ES 109	M00027717C:G05
ES 85	M00057091A:C04	ES 109	M00027733D:D05
ES 85	M00057091C:E12	ES 109	M00027742C:B01
ES 85	M00057093B:F09	ES 109	M00027742C:B01

ES 85	M00057099C:C08	ES 109	M00027747D:D01
ES 85	M00057100C:E09	ES 109	M00027757A:B06
ES 85	M00057100D:B03	ES 109	M00027781D:E04
ES 85	M00057103A:E11	ES 109	M00027786D:B01
ES 85	M00057103A:H09	ES 109	M00027803A:H10
ES 85	M00057104B:F08	ES 109	M00027806C:H05
ES 85	M00057106B:A03	ES 109	M00027808D:G10
ES 85	M00057106C:E02	ES 109	M00027817B:B11
ES 85	M00057106D:B06	ES 109	M00027820C:C02
ES 85	M00057108B:F04	ES 109	M00027823C:G07
ES 85	M00057108D:E09	ES 109	M00027829C:D02
ES 85	M00057108D:E09	ES 109	M00027833C:D01
ES 85	M00057112D:B09	ES 110	M00042345A:F12
ES 85	M00057114D:B10	ES 110	M00042523A:C05
ES 85	M00057117D:G11	ES 110	M00042523C:E08
ES 85	M00057118C:C02	ES 110	M00042525D:E01
ES 85	M00057120D:E12	ES 110	M00042527B:D07
ES 85	M00057124B:D10	ES 110	M00042528C:F11
ES 85	M00057127A:F11	ES 110	M00042529C:G07
ES 85	M00057127B:G07	ES 110	M00042532A:F08
ES 85	M00057130C:H11	ES 110	M00042534A:B07
ES 85	M00057131C:B01	ES 110	M00042536D:F01
ES 85	M00057132C:F08	ES 110	M00042537A:H05
ES 85	M00057133D:F01	ES 110	M00042538B:E06
ES 85	M00057134A:C01	ES 110	M00042538D:A08
ES 85	M00057134C:A01	ES 110	M00042539C:E05
ES 85	M00057134D:G10	ES 110	M00042540A:H06
ES 85	M00057135D:H04	ES 110	M00042540D:F03
ES 85	M00057136A:F01	ES 110	M00042540D:H05
ES 85	M00057141B:B02	ES 110	M00042543C:H02
ES 85	M00057141D:D02	ES 110	M00042544B:D02
ES 85	M00057142A:A07	ES 110	M00042544C:F10
ES 85	M00057143C:E05	ES 110	M00042547A:A02
ES 85	M00057145A:D05	ES 110	M00042547B:D11
ES 85	M00057146D:C09	ES 110	M00042547C:F02

ES 85	M00057147A:A01	ES 110	M00042551A:D09
ES 85	M00057150A:C10	ES 110	M00042556A:D04
ES 85	M00057151A:B04	ES 110	M00042563C:E02
ES 86	M00057154A:D06	ES 110	M00042563C:E02
ES 86	M00057154C:B04	ES 110	M00042563D:G09
ES 86	M00057161B:E09	ES 110	M00042564B:H11
ES 86	M00057162A:C07	ES 110	M00042565A:H03
ES 86	M00057162B:H02	ES 110	M00042565C:A08
ES 86	M00057162D:D10	ES 110	M00042567D:C01
ES 86	M00057163D:B01	ES 110	M00042570D:H02
ES 86	M00057165D:E12	ES 110	M00042573C:A07
ES 86	M00057167B:E12	ES 110	M00042574B:H08
ES 86	M00057167B:G12	ES 110	M00042575C:D01
ES 86	M00057167D:B07	ES 110	M00042693D:E04
ES 86	M00057170C:H03	ES 110	M00042694C:E02
ES 86	M00057174B:C06	ES 110	M00042695B:H05
ES 86	M00057174B:G12	ES 110	M00042700B:A01
ES 86	M00057174C:H12	ES 110	M00042700B:D03
ES 86	M00057180A:H11	ES 110	M00042700B:D03
ES 86	M00057181C:D06	ES 110	M00042700D:H05
ES 86	M00057182D:B11	ES 110	M00042704A:F04
ES 86	M00057189B:G05	ES 110	M00042704A:F09
ES 86	M00057191A:A03	ES 110	M00042704D:E02
ES 86	M00057192B:E02	ES 110	M00042705A:D02
ES 86	M00057192D:G02	ES 110	M00042706C:A04
ES 86	M00057196A:E03	ES 110	M00054596B:G11
ES 86	M00057196C:F04	ES 110	M00004101C:H01
ES 86	M00057203C:E06	ES 111	M00042711C:G11
ES 86	M00057208A:A02	ES 111	M00042711D:C04
ES 86	M00057208C:C06	ES 111	M00042712B:B10
ES 86	M00057208C:D08	ES 111	M00042717D:D04
ES 86	M00057211B:F07	ES 111	M00042718B:C03
ES 86	M00057211D:A06	ES 111	M00042720C:D06
ES 86	M00057215B:B02	ES 111	M00042720D:G10
ES 86	M00057217B:B07	ES 111	M00042721A:G07

ES 86	M00057218D:C01	ES 111	M00042727C:H12
ES 86	M00057223C:C06	ES 111	M00042728D:E07
ES 86	M00057224B:C10	ES 111	M00042732A:G09
ES 86	M00057226D:C05	ES 111	M00042735C:G02
ES 86	M00057229D:F06	ES 111	M00042735D:A07
ES 86	M00057230C:D12	ES 111	M00042738B:D10
ES 86	M00057231C:G09	ES 111	M00042739D:D01
ES 86	M00057231D:A09	ES 111	M00042741D:D10
ES 86	M00057232B:D06	ES 111	M00042742B:H03
ES 86	M00057233A:F07	ES 111	M00042742C:A06
ES 86	M00057233B:E04	ES 111	M00042742D:D05
ES 86	M00057236B:H06	ES 111	M00042746B:F02
ES 86	M00057237A:B11	ES 111	M00042746D:B09
ES 86	M00057239A:G08	ES 111	M00042750D:B09
ES 86	M00057241B:B04	ES 111	M00042881D:C08
ES 86	M00057242B:F07	ES 111	M00042883A:F12
ES 87	M00057242D:B09	ES 111	M00042886C:C03
ES 87	M00057242D:H05	ES 111	M00042886C:F01
ES 87	M00057249A:C06	ES 111	M00042887C:D07
ES 87	M00057259A:H10	ES 111	M00042889B:A09
ES 87	M00057259B:B08	ES 111	M00042890D:C08
ES 87	M00057266C:D04	ES 111	M00042891B:C04
ES 87	M00057266C:G12	ES 111	M00042893B:C08
ES 87	M00057268C:E10	ES 111	M00042900C:C07
ES 87	M00057270B:H09	ES 111	M00042901B:A03
ES 87	M00057270C:E04	ES 111	M00042902A:C04
ES 87	M00057271C:E01	ES 111	M00042905A:F11
ES 87	M00057272A:B03	ES 111	M00042905C:C10
ES 87	M00057272C:H04	ES 111	M00042908D:G01
ES 87	M00057272D:A01	ES 111	M00042909B:G04
ES 87	M00057275B:A12	ES 111	M00042911A:H03
ES 87	M00057277B:C09	ES 111	M00042914D:B10
ES 87	M00057277B:E10	ES 111	M00054792D:E09
ES 87	M00057279A:G02	ES 111	M00054793D:B07
ES 87	M00057280C:A06	ES 111	M00054798D:F01

ES 87	M00057283A:E06	ES 111	M00054913C:G03
ES 87	M00057288D:E08	ES 111	M00054915D:E07
ES 87	M00057291C:B06	ES 111	M00054917B:F09
ES 87	M00057297A:F03	ES 111	M00054917D:D12
ES 87	M00057300B:F02	ES 111	M00054918C:D03
ES 87	M00057301B:H12	ES 112	M00054918D:C11
ES 87	M00057304A:E01	ES 112	M00055426B:B02
ES 87	M00057306B:H07	ES 112	M00055426C:H06
ES 87	M00057312B:E11	ES 112	M00055427A:F01
ES 87	M00057318B:B09	ES 112	M00055428C:A02
ES 87	M00057318C:A03	ES 112	M00055429A:H05
ES 87	M00057324A:D12	ES 112	M00055430B:H02
ES 87	M00057325C:C10	ES 112	M00055431C:E09
ES 87	M00057333A:F09	ES 112	M00055438C:C06
ES 87	M00057334B:F01	ES 112	M00055438C:H10
ES 87	M00057337B:G02	ES 112	M00055441B:D02
ES 87	M00057340B:C12	ES 112	M00055445D:G06
ES 87	M00042355A:G02	ES 112	M00055446C:B06
ES 87	M00042355D:C01	ES 112	M00055447D:H04
ES 87	M00042442D:A02	ES 112	M00055447D:H04
ES 87	M00042444D:G05	ES 112	M00055448A:D08
ES 87	M00042444D:H08	ES 112	M00055448C:E07
ES 87	M00042450D:H10	ES 112	M00055450A:G09
ES 87	M00042453C:E01	ES 112	M00055450D:B08
ES 87	M00042460D:A07	ES 112	M00055451A:F07
ES 87	M00042517C:F07	ES 112	M00055451A:F11
ES 87	M00042518D:A06	ES 112	M00055451C:G11
ES 87	M00042520A:F04	ES 112	M00055453C:E01
ES 88	M00042520A:F09	ES 112	M00055453C:E01
ES 88	M00042520A:F09	ES 112	M00055454A:A07
ES 88	M00043296C:B10	ES 112	M00055454A:H11
ES 88	M00043300A:H11	ES 112	M00055454C:G05
ES 88	M00043301A:F06	ES 112	M00055456D:F12
ES 88	M00043301D:H09	ES 112	M00055463D:H10
ES 88	M00043304A:D01	ES 112	M00055464A:F05

ES 88	M00043304B:C05	ES 112	M00055466D:B08
ES 88	M00043304B:C05	ES 112	M00055470B:G01
ES 88	M00043306D:B07	ES 112	M00055491A:G08
ES 88	M00043309B:H07	ES 112	M00055494D:C09
ES 88	M00043310C:B03	ES 112	M00055495A:G02
ES 88	M00043313A:A03	ES 112	M00055495C:D05
ES 88	M00043313A:G07	ES 112	M00055495C:F03
ES 88	M00043313D:C06	ES 112	M00055495D:E02
ES 88	M00043314C:H04	ES 112	M00055496A:F09
ES 88	M00043317A:H01	ES 112	M00055496B:E07
ES 88	M00043317C:F04	ES 112	M00055496C:C09
ES 88	M00043323C:D04	ES 112	M00055498A:H09
ES 88	M00043324D:D04	ES 112	M00055500D:B05
ES 88	M00043327D:H02	ES 112	M00055504C:D08
ES 88	M00043327D:H02	ES 112	M00055505D:A10
ES 88	M00043336B:E08	ES 112	M00055508D:E03
ES 88	M00043338A:B03	ES 112	M00055509C:H09
ES 88	M00043338B:A03	ES 112	M00055510B:B07
ES 88	M00043345B:C03	ES 113	M00055511D:E09
ES 88	M00043347B:G12	ES 113	M00055512C:G06
ES 88	M00043349A:C08	ES 113	M00055512D:D07
ES 88	M00043350B:H06	ES 113	M00055512D:F08
ES 88	M00043350C:H09	ES 113	M00055513C:D06
ES 88	M00043352A:E09	ES 113	M00055514D:H05
ES 88	M00043352D:B05	ES 113	M00055516B:E08
ES 88	M00043354D:C01	ES 113	M00055517B:D03
ES 88	M00043355D:H11	ES 113	M00055519B:C06
ES 88	M00043361D:D05	ES 113	M00055519C:H07
ES 88	M00043365A:C06	ES 113	M00055520C:A06
ES 88	M00043374A:B02	ES 113	M00055522A:E07
ES 88	M00043374B:B06	ES 113	M00055522D:C02
ES 88	M00043377A:C03	ES 113	M00055522D:C02
ES 88	M00043379D:C07	ES 113	M00055523D:C03
ES 88	M00043381B:E10	ES 113	M00055525C:B07
ES 88	M00043386D:A06	ES 113	M00055526D:F09

ES 88	M00043388D:C09	ES 113	M00055527C:E02
ES 88	M00043394D:B06	ES 113	M00055527C:E04
ES 88	M00043397B:B02	ES 113	M00055527D:G11
ES 88	M00043397C:B09	ES 113	M00055528C:F06
ES 88	M00043503C:C08	ES 113	M00055529D:B02
ES 88	M00043503C:E05	ES 113	M00055530D:B07
ES 89	M00043504C:G06	ES 113	M00055532C:G08
ES 89	M00043504D:G08	ES 113	M00055534C:H01
ES 89	M00043506A:H09	ES 113	M00055536C:E06
ES 89	M00043507A:D05	ES 113	M00055536C:F03
ES 89	M00043508A:A08	ES 113	M00055538B:H11
ES 89	M00043508D:C01	ES 113	M00055542C:C01
ES 89	M00054486A:B11	ES 113	M00055542C:F06
ES 89	M00054493A:A10	ES 113	M00055542D:A09
ES 89	M00054494A:E01	ES 113	M00055543A:C05
ES 89	M00054496A:B09	ES 113	M00055543A:C05
ES 89	M00054499B:E11	ES 113	M00055543C:G08
ES 89	M00054499B:E11	ES 113	M00055544A:E04
ES 89	M00054502A:D01	ES 113	M00055544B:B02
ES 89	M00054502C:E02	ES 113	M00055545C:H12
ES 89	M00054507A:C11	ES 113	M00055547D:D10
ES 89	M00054510D:H09	ES 113	M00055547D:E05
ES 89	M00054513A:A12	ES 113	M00055548A:F04
ES 89	M00054518D:D03	ES 113	M00055548C:E12
ES 89	M00054520C:B05	ES 113	M00055548C:E12
ES 89	M00054521D:F04	ES 113	M00055552A:C09
ES 89	M00054522B:H11	ES 113	M00055553B:H04
ES 89	M00054523D:A10	ES 113	M00055553D:C07
ES 89	M00054524D:B02	ES 113	M00055553D:H02
ES 89	M00054534D:D02	ES 113	M00055556C:H09
ES 89	M00054535C:H09	ES 113	M00055560B:B12
ES 89	M00054542C:A08	ES 114	M00055560B:F02
ES 89	M00054551C:G03	ES 114	M00055560C:F06
ES 89	M00054555C:G12	ES 114	M00055563A:A02
ES 89	M00054561D:E06	ES 114	M00055572A:B12

ES 89	M00054563B:C09	ES 114	M00055572C:F03
ES 89	M00054568A:G11	ES 114	M00055575A:D08
ES 89	M00054569A:H07	ES 114	M00055578A:H09
ES 89	M00054571C:C01	ES 114	M00055581D:B01
ES 89	M00054572B:C01	ES 114	M00055582B:E04
ES 89	M00054575C:C01	ES 114	M00055583B:B04
ES 89	M00054580C:D11	ES 114	M00055583B:H05
ES 89	M00054583A:F05	ES 114	M00055584A:C11
ES 89	M00054587A:F09	ES 114	M00055584D:G06
ES 89	M00054590C:G02	ES 114	M00055586C:F05
ES 89	M00054591C:H07	ES 114	M00055586D:F02
ES 89	M00054595A:B02	ES 114	M00055591C:H01
ES 89	M00054595B:H09	ES 114	M00055592D:A05
ES 89	M00054596B:B07	ES 114	M00055594B:A01
ES 89	M00054600D:G07	ES 114	M00055597C:E08
ES 89	M00054601A:H10	ES 114	M00055601C:D09
ES 89	M00054601D:E08	ES 114	M00055602B:G10
ES 89	M00054602A:C04	ES 114	M00055602C:E07
ES 90	M00054602B:D02	ES 114	M00055609A:G03
ES 90	M00054604A:D09	ES 114	M00055609D:F12
ES 90	M00054604A:D09	ES 114	M00055613A:D10
ES 90	M00054605C:D01	ES 114	M00055613A:E02
ES 90	M00054609A:F01	ES 114	M00055618C:A06
ES 90	M00054609D:H06	ES 114	M00055628A:A08
ES 90	M00054611C:F02	ES 114	M00055630B:E09
ES 90	M00054613A:D09	ES 114	M00055633D:A02
ES 90	M00054613A:D09	ES 114	M00055633D:G11
ES 90	M00054617B:A09	ES 114	M00055635A:H10
ES 90	M00054621B:C06	ES 114	M00055635B:E10
ES 90	M00054621D:D11	ES 114	M00055635C:G04
ES 90	M00054629C:E09	ES 114	M00055636A:F10
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ES 90	M00054636C:A02	ES 114	M00055653A:H04
ES 90	M00054636C:F02	ES 114	M00055656A:E09
ES 90	M00054638A:D09	ES 114	M00055662C:A04

ES 90	M00054638B:C08	ES 114	M00055664C:A08
ES 90	M00054646C:B01	ES 114	M00055668B:B07
ES 90	M00054647D:H02	ES 114	M00055679A:A07
ES 90	M00054648C:H10	ES 114	M00055681B:G02
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ES 90	M00054706B:C09	ES 115	M00055704C:D07
ES 90	M00054707B:B08	ES 115	M00055705C:G07
ES 90	M00054707B:E05	ES 115	M00055706A:A01
ES 90	M00054713A:D12	ES 115	M00055706B:G01
ES 90	M00054720D:D12	ES 115	M00055707D:C08
ES 90	M00054720D:F11	ES 115	M00055709B:G09
ES 90	M00054721C:F11	ES 115	M00055716C:B04
ES 90	M00054722C:D01	ES 115	M00055717B:F04
ES 90	M00054722D:C08	ES 115	M00055718A:F05
ES 90	M00054726A:F08	ES 115	M00055720B:G09
ES 90	M00054727D:E10	ES 115	M00055720C:A06
ES 90	M00054727D:H06	ES 115	M00055720D:A01
ES 90	M00054728B:E08	ES 115	M00055721B:F06
ES 91	M00054728D:B10	ES 115	M00055721B:F06
ES 91	M00054729A:E01	ES 115	M00055721C:E05
ES 91	M00054731C:C12	ES 115	M00055723A:B08
ES 91	M00054732D:E03	ES 115	M00055723D:E05

ES 91	M00054734D:H10	ES 115	M00055724D:D09
ES 91	M00054739A:G03	ES 115	M00055726B:B08
ES 91	M00054739C:D03	ES 115	M00055726C:D12
ES 91	M00054739C:E06	ES 115	M00055726C:G10
ES 91	M00054740A:H08	ES 115	M00055729D:A06
ES 91	M00054741A:C10	ES 115	M00055731A:H12
ES 91	M00054741A:E10	ES 115	M00055733A:G11
ES 91	M00054741D:G10	ES 115	M00055734C:H05
ES 91	M00054743C:E02	ES 115	M00055735C:C07
ES 91	M00054745D:A03	ES 115	M00055735C:G05
ES 91	M00054747A:F01	ES 115	M00055736A:D06
ES 91	M00054747D:C06	ES 115	M00055736B:G03
ES 91	M00054750C:D12	ES 115	M00055736C:G07
ES 91	M00054752B:A07	ES 115	M00055740B:B12
ES 91	M00054755B:H06	ES 115	M00055740B:F09
ES 91	M00054759A:B08	ES 115	M00055743B:C12
ES 91	M00054760A:A12	ES 115	M00055744B:C08
ES 91	M00054762B:F07	ES 115	M00055744C:F08
ES 91	M00054765B:C05	ES 115	M00055744C:F09
ES 91	M00054766C:B04	ES 115	M00055744D:G08
ES 91	M00054769A:F07	ES 115	M00055747C:D09
ES 91	M00054772C:C06	ES 115	M00055749D:H11
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ES 91	M00054776B:F01	ES 116	M00055755C:D02
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ES 98	M00005516D:H06	ES 126	M00056505B:H02
ES 98	M00005517B:F04	ES 126	M00056505D:D07
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ES 105	M00022151A:D11	ES 132	M00056964B:A02
ES 105	M00022151A:G05	ES 132	M00056966D:A11
ES 105	M00022163A:C08	ES 132	M00056967A:D02
ES 105	M00022598B:E12	ES 132	M00056967A:E07
ES 105	M00022598C:D05	ES 132	M00056969B:C08
ES 105	M00022617B:C02	ES 132	M00056969D:B01
ES 105	M00022624C:C02	ES 132	M00056972A:F05
ES 105	M00022641A:C10	ES 132	M00056973D:B08
ES 105	M00022641A:E06	ES 132	M00056974C:F04
ES 105	M00022641B:F02	ES 132	M00056976C:F10
ES 105	M00022645D:A05	ES 132	M00056977A:G03
ES 105	M00022645D:C07	ES 132	M00056985B:C05
ES 105	M00022651D:B04	ES 132	M00056986A:F11
ES 105	M00022651D:C01	ES 132	M00056986D:G01
ES 105	M00022655A:D10	ES 132	M00056990C:B09
ES 105	M00022656D:E11	ES 132	M00056990D:C11
ES 105	M00022660A:B04	ES 132	M00056993A:B06
ES 105	M00022667A:C05	ES 132	M00056993D:D03
ES 105	M00022667D:E11	ES 132	M00056994B:F07
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ES 105	M00022702B:B04	ES 133	M00056997C:H09
ES 105	M00022716C:C06	ES 133	M00056998A:E08
ES 105	M00022716C:C06	ES 133	M00057002D:B05
ES 105	M00022719A:F12	ES 133	M00057002D:B06

ES 105	M00022720B:A11	ES 133	M00057003B:B09
ES 105	M00022720C:C09	ES 133	M00057005B:C01
ES 105	M00022724C:D04	ES 133	M00057005C:D03
ES 105	M00022738B:D06	ES 133	M00057007C:B12
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ES 105	M00022745C:C07	ES 133	M00057011A:D03
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ES 105	M00022750A:A07	ES 133	M00057015A:C12
ES 105	M00022791B:F11	ES 133	M00057019C:H02
ES 105	M00022813B:A08	ES 133	M00057023A:H09
ES 105	M00022820D:C06	ES 133	M00057024A:E02
ES 105	M00022823A:D03	ES 133	M00057024A:G05
ES 105	M00022828A:C06	ES 133	M00057024D:H08
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ES 105	M00022829C:H10	ES 133	M00057027C:G06
ES 105	M00022831B:H07	ES 133	M00057028D:D09
ES 106	M00022831C:A09	ES 133	M00057029A:C12
ES 106	M00022831D:C04	ES 133	M00057029D:A06
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ES 106	M00022836A:G03	ES 133	M00057035B:C09
ES 106	M00022853C:C11	ES 133	M00057041D:B11
ES 106	M00022861D:B10	ES 133	M00057044C:F06
ES 106	M00022872A:B05	ES 133	M00057047B:C02
ES 106	M00022876B:B05	ES 133	M00057049A:G06
ES 106	M00022876D:D08	ES 133	M00057049C:H05
ES 106	M00022880C:G09	ES 133	M00057052D:B11
ES 106	M00022892C:G07	ES 133	M00057052D:G09
ES 106	M00022895B:B11	ES 133	M00057055B:G08
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ES 106	M00022901D:E11	ES 133	M00057060B:A12
ES 106	M00022902C:H10	ES 133	M00057061C:D04
ES 106	M00022908B:H03	ES 133	M00057063A:C08

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ES 106	M00022934D:B03	ES 133	M00057070D:B08
ES 106	M00022956B:B09	ES 133	M00057072B:E02
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ES 106	M00022973A:G07	ES 133	M00057074D:C09
ES 106	M00022973C:G08	ES 133	M00057074D:C09
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ES 106	M00022997A:C08	ES 134	M00055911B:E06
ES 106	M00022998B:C08	ES 134	M00055912C:E10
ES 106	M00023002D:G10	ES 134	M00055912D:C05
ES 106	M00023015A:D10	ES 134	M00055913B:D05
ES 106	M00023015C:D02	ES 134	M00055919A:A06
ES 106	M00023020D:G09	ES 134	M00055921A:E03
ES 106	M00023023C:F03	ES 134	M00055921B:B11
ES 106	M00023029A:E06	ES 134	M00055922A:C02
ES 106	M00023331D:A11	ES 134	M00055924A:H11
ES 106	M00023347D:C12	ES 134	M00055930A:B08
ES 106	M00023377D:C09	ES 134	M00055931A:A03
ES 106	M00023393D:C02	ES 134	M00055931A:C01
ES 106	M00023393D:E12	ES 134	M00055931B:E01
ES 106	M00023399C:C08	ES 134	M00055936B:E07
ES 106	M00023409A:G08	ES 134	M00055937B:C02
ES 106	M00023414B:F03	ES 134	M00055941B:B12
ES 106	M00023428C:D03	ES 134	M00055941B:B12
ES 106	M00023428D:F11	ES 134	M00055945A:H11
ES 106	M00023430B:D10	ES 134	M00055945B:E10
ES 106	M00023518C:A04	ES 134	M00055946D:G07
ES 107	M00023520A:G07	ES 134	M00055951C:C02
ES 107	M00026804D:D03	ES 134	M00055956C:E02
ES 107	M00026805B:B04	ES 134	M00055958D:F02
ES 107	M00026848C:G11	ES 134	M00055959D:A12
ES 107	M00026854A:E07	ES 134	M00055966C:A03
ES 107	M00026856C:C11	ES 134	M00055966C:D06

ES 107	M00026860D:E01	ES 134	M00055971C:E07
ES 107	M00026861D:A09	ES 134	M00055973A:D04
ES 107	M00026865D:G11	ES 134	M00055976B:F01
ES 107	M00026866A:H08	ES 134	M00055979B:B09
ES 107	M00026873B:E11	ES 134	M00055980A:A10
ES 107	M00026873D:B08	ES 134	M00055981D:A07
ES 107	M00026879A:B02	ES 134	M00055984C:C02
ES 107	M00026879C:D10	ES 134	M00055985D:D01
ES 107	M00026890C:D02	ES 134	M00055990C:B05
ES 107	M00026893C:A01	ES 134	M00055992C:E11
ES 107	M00026896D:E10	ES 134	M00056139D:E04
ES 107	M00026899C:G11	ES 134	M00056139D:G01
ES 107	M00026899C:G11	ES 134	M00056140B:H07
ES 107	M00026900B:C02	ES 134	M00056140D:E07
ES 107	M00026902A:G04	ES 134	M00056141A:D05
ES 107	M00026906B:C10	ES 134	M00056141D:B09
ES 107	M00026909A:G03	ES 134	M00056143A:E09
ES 107	M00026917D:H03	ES 134	M00056144B:C09
ES 107	M00026926D:C05	ES 134	M00056145C:B04
ES 107	M00026934D:E09	ES 134	M00056149C:B01
ES 107	M00026936D:C12	ES 135	M00056150B:C12
ES 107	M00026937C:B08	ES 135	M00056153C:D01
ES 107	M00026938A:F04	ES 135	M00056156D:A12
ES 107	M00026938A:F04	ES 135	M00056160D:A08
ES 107	M00026949B:H10	ES 135	M00056161D:G04
ES 107	M00026950A:F12	ES 135	M00056162B:F08
ES 107	M00026950D:H01	ES 135	M00056162B:F08
ES 107	M00026951A:G06	ES 135	M00056162D:D06
ES 107	M00026951A:G11	ES 135	M00056162D:E09
ES 107	M00026951A:G11	ES 135	M00056167D:B08
ES 107	M00026951C:D03	ES 135	M00056169A:F06
ES 107	M00026975C:B03	ES 135	M00056171C:H11
ES 107	M00026977A:E09	ES 135	M00056171C:H12
ES 107	M00026984A:D10	ES 135	M00056180B:H09
ES 107	M00026985C:B05	ES 135	M00056184B:D08

ES 107	M00026986B:H10	ES 135	M00056184C:H03
ES 107	M00026993B:H06	ES 135	M00056184D:F01
ES 107	M00026994C:A07	ES 135	M00056185D:A03
ES 107	M00026996D:A06	ES 135	M00056185D:D06
ES 107	M00027000C:F05	ES 135	M00056186C:F02
ES 107	M00027006B:H01	ES 135	M00056190D:G02
ES 107	M00027013D:E10	ES 135	M00056192D:E04
ES 108	M00027014C:G04	ES 135	M00056192D:H02
ES 108	M00027014D:G04	ES 135	M00056195B:C08
ES 108	M00027016D:G06	ES 135	M00056198A:D07
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ES 108	M00027028D:C07	ES 135	M00056201C:H08
ES 108	M00027030C:C08	ES 135	M00056203A:H10
ES 108	M00027034B:D09	ES 135	M00056204B:A04
ES 108	M00027034C:D11	ES 135	M00056205B:D01
ES 108	M00027035D:H09	ES 135	M00056206A:E06
ES 108	M00027039A:F06	ES 136	M00055997C:G11
ES 108	M00027039B:E09	ES 136	M00055999C:G10
ES 108	M00027042C:G11	ES 136	M00055999D:G06
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ES 108	M00027054B:B03	ES 136	M00056001A:B06
ES 108	M00027076D:F07	ES 136	M00056001A:B07
ES 108	M00027084C:H10	ES 136	M00056001C:E09
ES 108	M00027088D:H06	ES 136	M00056003A:E06
ES 108	M00027090A:E08	ES 136	M00056005B:E05
ES 108	M00027093C:B08	ES 136	M00056005D:C04
ES 108	M00027096A:G07	ES 136	M00056007A:A11
ES 108	M00027097C:G11	ES 136	M00056007C:F06
ES 108	M00027111A:H04	ES 136	M00056016D:D06
ES 108	M00027134A:G02	ES 136	M00056018B:G05
ES 108	M00027139D:C06	ES 136	M00056020A:D10
ES 108	M00027140A:C11	ES 136	M00056020D:D07
ES 108	M00027163A:D11	ES 136	M00056028C:F03
ES 108	M00027165C:F11	ES 136	M00056036D:B06

ES 108	M00027168C:H10	ES 136	M00056037C:B02
ES 108	M00027171D:B07	ES 136	M00056038D:F04
ES 108	M00027172A:C03	ES 136	M00056041A:C04
ES 108	M00027173D:D08	ES 136	M00056042A:A01
ES 108	M00027183B:B01	ES 136	M00056045D:H01
ES 108	M00027193C:C05	ES 136	M00056050C:A03
ES 108	M00027194D:A05	ES 136	M00056053A:A09
ES 108	M00027197A:G07	ES 136	M00056053A:D12
ES 108	M00027197B:F07	ES 136	M00056055A:A07
ES 108	M00027203B:H08	ES 136	M00056055B:B01
ES 108	M00027207B:E09	ES 136	M00056055C:D03
ES 108	M00027217A:G03	ES 136	M00056058A:H04
ES 108	M00027220A:B12	ES 136	M00056060B:B10
ES 108	M00027222A:C09	ES 136	M00056061B:F06
ES 108	M00027229D:E06	ES 136	M00056066D:H07
ES 108	M00027231D:A03	ES 136	M00056067B:D08
ES 108	M00027524B:B11	ES 136	M00056074D:G10
ES 108	M00027527A:G04	ES 136	M00056077D:E06
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ES 108	M00027535D:E08	ES 136	M00056077D:E12
ES 109	M00027536D:G12	ES 136	M00056079B:D12
ES 109	M00027543C:B09	ES 136	M00056079B:F07
ES 109	M00027543D:G07	ES 136	M00056079C:C11
ES 109	M00027556D:G10	ES 136	M00056081D:B05
ES 109	M00027561C:C04	ES 136	M00056081D:B09
ES 109	M00027562B:C02	ES 136	M00056082C:F06
ES 109	M00027564A:D03	ES 136	M00056085D:H11
ES 109	M00027571C:C11	ES 136	M00056094A:H07
ES 109	M00027573A:F09	ES 136	M00056098A:H01
ES 109	M00027578B:F05	ES 136	M00056099B:G09
ES 109	M00027578C:E04	ES 136	M00056099B:H11
ES 109	M00027580C:E10	ES 136	M00056099B:H11
ES 109	M00027581B:E01	ES 136	M00056103A:D12
ES 109	M00027588A:C01	ES 136	M00056103C:H12
ES 109	M00027588C:A06	ES 136	M00056107B:E06

ES 109	M00027594B:C03	ES 136	M00056108D:B12
ES 109	M00027604A:G10	ES 136	M00056108D:B12
ES 109	M00027604A:G10	ES 136	M00056110C:D09
ES 109	M00027605C:E05	ES 136	M00056111D:H02
ES 109	M00027607A:H05	ES 136	M00056112A:H02
ES 109	M00027608C:H07	ES 136	M00056114C:C06
ES 109	M00027616C:G12	ES 136	M00056125B:D09
ES 109	M00027628C:A01	ES 136	M00056128C:B10
ES 109	M00027639B:E11	ES 136	M00056131B:C12
ES 109	M00027641B:A01	ES 136	M00056133D:D09
ES 109	M00027652B:G03	ES 136	M00056136A:B11

The above material has been deposited with the American Type Culture Collection, Rockville, Maryland, under the accession number indicated. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. The deposit will be maintained for a period of at least 30 years following issuance of this patent, or for the enforceable life of the patent, whichever is greater. Upon the granting of a patent, all restrictions on the availability to the public of the deposited material will be irrevocably removed.

The deposits described herein are provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific

clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Example 77: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

cDNA libraries were constructed from mRNA isolated from the GRRpz or and
5 WOca cells, which were provided by Dr. Donna M. Peehl, Department of Medicine,
Stanford University School of Medicine. GRRpz cells were primary cells derived from
normal prostate epithelium. The WOca cells were prostate epithelial cells derived from
prostate cancer Gleason Grade 4+4. Polynucleotides expressed by these cells were isolated
and analyzed; the sequences of these polynucleotides were about 275-300 nucleotides in
10 length.

The sequences of the isolated polynucleotides were first masked to eliminate low
complexity sequences using the XBLAST masking program (Claverie "Effective Large-
Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular
Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY
15 (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis
Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and
Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the
final search results, except to eliminate sequences of relative little interest due to their low
complexity, and to eliminate multiple "hits" based on similarity to repetitive regions
20 common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used
in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap,
99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this
search also were discarded if the inclusive parameters were met, but the sequence was
ribosomal or vector-derived.

25 The resulting sequences from the previous search were classified into three groups
(1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database
search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than
45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60%
overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having
30 greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were
discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and
high similarity (parameters as above). Two searches were performed on these sequences.

First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 316 sequences listed as SEQ ID NOS:15667-15982 in the accompanying Sequence Listing and summarized in Table 120 (inserted prior to claims). Each identified polynucleotide represents sequence from at least a partial mRNA transcript. Many of the sequences include the sequence ggcaacgag at the 5' end; this sequence is a sequencing artifact and not part of the sequence of the polynucleotides of the invention.

Table 120 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER"); 3) the sequence name ("SEQ NAME") used as an internal identifier of the sequence; 4) the orientation of the sequence ("ORIENT"); 5) the name assigned to the clone from which the sequence was isolated ("CLONE ID"); and the name of the library from which the sequence was isolated ("LIBRARY"). CH22PRC indicates the sequence was isolated from Library 22; CH21PRN indicates the sequence was isolated from Library 21. A description of the libraries is provided in Table 122 below. Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

Example 78: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS: 15667-15982 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs, available over the world wide web at a saite

sponsored by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health (see also Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the
5 XBLAST program for masking low complexity as described above in Example 77.

Table 121 (inserted before the claims) provide the alignment summaries having a p value of 1×10^{-2} or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Specifically, Table 121 provides the SEQ ID NO of the query sequence, the accession number of the GenBank
10 database entry of the homologous sequence, and the p value of the alignment. Table 121 also provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous sequence, and the p value of the alignment. The alignments provided in Table 121 are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification. The
15 activity of the polypeptide encoded by the SEQ ID NOS listed in Table 121 can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and
20 functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and actual activities and functions of the nearest neighbor sequences listed in Table 121 and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also
25 indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the corresponding
30 polynucleotides.

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
15667	819545	RTA22200265F.k.06.1.P.Seq	F	M00064554D:A03	CH22PRC
15668	377944	RTA22200251F.j.02.1.P.Seq	F	M00063482A:A08	CH21PRN
15669	818497	RTA22200252F.a.13.1.P.Seq	F	M00063514C:D03	CH21PRN
15670	819498	RTA22200252F.n.05.1.P.Seq	F	M00063638C:G12	CH21PRN
15671	455465	RTA22200264F.e.16.1.P.Seq	F	M00064454A:H10	CH22PRC
15672	819069	RTA22200255F.f.01.1.P.Seq	F	M00063940D:F09	CH21PRN
15673	672003	RTA22200265F.b.09.1.P.Seq	F	M00064517C:F11	CH22PRC
15674	728115	RTA22200253F.o.24.1.P.Seq	F	M00063838B:G08	CH21PRN
15675	372700	RTA22200260F.b.20.1.P.Seq	F	M00063580C:A06	CH22PRC
15676	818056	RTA22200266F.c.13.1.P.Seq	F	M00064593D:C01	CH22PRC
15677	818497	RTA22200255F.a.17.1.P.Seq	F	M00063920D:H02	CH21PRN
15678	729832	RTA22200267F.l.21.1.P.Seq	F	M00064714A:G03	CH22PRC
15679	505514	RTA22200251F.b.21.1.P.Seq	F	M00063158A:A01	CH21PRN
15680	376488	RTA22200254F.c.05.1.P.Seq	F	M00063852B:D08	CH21PRN
15681	376488	RTA22200260F.b.09.1.P.Seq	F	M00063578C:A06	CH22PRC
15682	748572	RTA22200254F.c.07.1.P.Seq	F	M00063852D:F07	CH21PRN
15683	549934	RTA22200253F.k.18.1.P.Seq	F	M00063801B:D04	CH21PRN
15684	819069	RTA22200255F.e.24.1.P.Seq	F	M00063940D:F09	CH21PRN
15685	817618	RTA22200253F.n.16.1.P.Seq	F	M00063828D:E05	CH21PRN
15686	124396	RTA22200263F.a.11.2.P.Seq	F	M00064375B:G07	CH22PRC
15687	404375	RTA22200260F.m.08.1.P.Seq	F	M00063967D:G02	CH22PRC
15688	391820	RTA22200261F.f.02.1.P.Seq	F	M00064000B:C03	CH22PRC
15689	672003	RTA22200267F.i.06.1.P.Seq	F	M00064693D:F08	CH22PRC
15690	830620	RTA22200263F.n.09.1.P.Seq	F	M00064424B:C12	CH22PRC
15691	450399	RTA22200251F.f.23.1.P.Seq	F	M00063467D:H07	CH21PRN
15692	450982	RTA22200261F.n.18.1.P.Seq	F	M00064307B:G02	CH22PRC
15693	819894	RTA22200264F.h.18.1.P.Seq	F	M00064467B:D06	CH22PRC
15694	379302	RTA22200257F.j.02.3.P.Seq	F	M00064178C:C04	CH21PRN
15695	379746	RTA22200256F.e.16.1.P.Seq	F	M00064086C:E01	CH21PRN
15696	124863	RTA22200265F.m.06.1.P.Seq	F	M00064564A:C02	CH22PRC
15697	379154	RTA22200257F.c.11.1.P.Seq	F	M00064151B:C07	CH21PRN
15698	830620	RTA22200262F.l.23.1.P.Seq	F	M00064358C:D09	CH22PRC
15699	389409	RTA22200266F.l.24.1.P.Seq	F	M00064631A:C07	CH22PRC
15700	397284	RTA22200262F.i.22.1.P.Seq	F	M00064346C:B09	CH22PRC
15701	819440	RTA22200264F.e.19.1.P.Seq	F	M00064454C:B06	CH22PRC
15702	389409	RTA22200266F.m.01.1.P.Seq	F	M00064631A:C07	CH22PRC
15703	518848	RTA22200265F.n.15.1.P.Seq	F	M00064571C:C04	CH22PRC
15704	830620	RTA22200263F.a.21.1.P.Seq	F	M00064376A:A05	CH22PRC
15705	379154	RTA22200256F.f.20.1.P.Seq	F	M00064090D:D09	CH21PRN
15706	818544	RTA22200256F.h.04.1.P.Seq	F	M00064105B:A03	CH21PRN
15707	817375	RTA22200251F.a.15.1.P.Seq	F	M00063152C:B07	CH21PRN

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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15709	817503	RTA22200266F.k.11.1.P.Seq	F	M00064624D:C09	CH22PRC
15710	377696	RTA22200256F.d.21.1.P.Seq	F	M00064082D:D10	CH21PRN
15711	375596	RTA22200261F.h.10.1.P.Seq	F	M00064009A:C01	CH22PRC
15712	817689	RTA22200263F.h.05.1.P.Seq	F	M00064399A:E01	CH22PRC
15713	831867	RTA22200262F.i.15.2.P.Seq	F	M00064345A:A03	CH22PRC
15714	830085	RTA22200261F.k.14.1.P.Seq	F	M00064293D:B12	CH22PRC
15715	389627	RTA22200264F.c.10.1.P.Seq	F	M00064447B:C06	CH22PRC
15716	397284	RTA22200259F.k.09.1.P.Seq	F	M00063555B:D01	CH22PRC
15717	380063	RTA22200261F.j.02.1.P.Seq	F	M00064014D:H05	CH22PRC
15718	830931	RTA22200266F.m.23.1.P.Seq	F	M00064633C:A03	CH22PRC
15719	819321	RTA22200257F.l.03.3.P.Seq	F	M00064194C:D02	CH21PRN
15720	475587	RTA22200261F.c.01.1.P.Seq	F	M00063990A:D05	CH22PRC
15721	819046	RTA22200255F.a.18.1.P.Seq	F	M00063920D:H05	CH21PRN
15722	817477	RTA22200253F.g.21.1.P.Seq	F	M00063784A:H12	CH21PRN
15723	475587	RTA22200261F.b.24.1.P.Seq	F	M00063990A:D05	CH22PRC
15724	728115	RTA22200253F.p.01.1.P.Seq	F	M00063838B:G08	CH21PRN
15725	389627	RTA22200260F.i.24.1.P.Seq	F	M00063957A:E02	CH22PRC
15726	403453	RTA22200256F.i.24.1.P.Seq	F	M00064113B:C04	CH21PRN
15727	508525	RTA22200255F.d.10.1.P.Seq	F	M00063931B:F07	CH21PRN
15728	819525	RTA22200261F.n.20.1.P.Seq	F	M00064307C:G03	CH22PRC
15729	817618	RTA22200255F.i.03.1.P.Seq	F	M00064025D:H12	CH21PRN
15730	819403	RTA22200254F.h.14.1.P.Seq	F	M00063888D:D05	CH21PRN
15731	553242	RTA22200254F.g.20.1.P.Seq	F	M00063886A:B06	CH21PRN
15732	817417	RTA22200255F.a.10.1.P.Seq	F	M00063919C:E07	CH21PRN
15733	817618	RTA22200252F.f.13.1.P.Seq	F	M00063604A:B11	CH21PRN
15734	611440	RTA22200262F.e.04.2.P.Seq	F	M00064328B:H09	CH22PRC
15735	817375	RTA22200260F.m.06.1.P.Seq	F	M00063967C:A12	CH22PRC
15736	213577	RTA22200255F.i.23.1.P.Seq	F	M00064033C:C11	CH21PRN
15737	820061	RTA22200265F.p.10.1.P.Seq	F	M00064579D:E11	CH22PRC
15738	455264	RTA22200259F.m.06.1.P.Seq	F	M00063559D:G03	CH22PRC
15739	455264	RTA22200255F.o.23.1.P.Seq	F	M00064059A:C11	CH21PRN
15740	380331	RTA22200255F.b.19.1.P.Seq	F	M00063926A:H04	CH21PRN
15741	380331	RTA22200252F.b.19.1.P.Seq	F	M00063518D:A01	CH21PRN
15742	817455	RTA22200267F.o.01.1.P.Seq	F	M00064723D:H03	CH22PRC
15743	423967	RTA22200252F.a.20.1.P.Seq	F	M00063515B:H02	CH21PRN
15744	220584	RTA22200261F.m.14.1.P.Seq	F	M00064302A:D10	CH22PRC
15745	817688	RTA22200251F.e.20.1.P.Seq	F	M00063462D:D07	CH21PRN
15746	549934	RTA22200253F.n.10.1.P.Seq	F	M00063826A:D03	CH21PRN
15747	819149	RTA22200255F.e.16.1.P.Seq	F	M00063938B:H07	CH21PRN
15748	817455	RTA22200267F.n.24.1.P.Seq	F	M00064723D:H03	CH22PRC

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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15750	830146	RTA22200260F.b.07.1.P.Seq	F	M00063578B:E02	CH22PRC
15751	194490	RTA22200264F.l.07.1.P.Seq	F	M00064481C:F03	CH22PRC
15752	819460	RTA22200257F.m.15.3.P.Seq	F	M00064200D:E08	CH21PRN
15753	819018	RTA22200257F.p.01.3.P.Seq	F	M00064212D:E04	CH21PRN
15754	830620	RTA22200259F.p.24.1.P.Seq	F	M00063571B:G03	CH22PRC
15755	141079	RTA22200262F.k.19.1.P.Seq	F	M00064354A:A10	CH22PRC
15756	376588	RTA22200256F.e.04.1.P.Seq	F	M00064083D:E05	CH21PRN
15757	380604	RTA22200264F.g.05.1.P.Seq	F	M00064460C:B01	CH22PRC
15758	413138	RTA22200260F.b.05.1.P.Seq	F	M00063577C:C02	CH22PRC
15759	818544	RTA22200265F.e.12.1.P.Seq	F	M00064527A:H07	CH22PRC
15760	647435	RTA22200257F.h.08.1.P.Seq	F	M00064172C:A02	CH21PRN
15761	551785	RTA22200266F.c.09.1.P.Seq	F	M00064593A:A05	CH22PRC
15762	17092	RTA22200261F.f.17.1.P.Seq	F	M00064002C:F06	CH22PRC
15763	818326	RTA22200251F.i.06.1.P.Seq	F	M00063478C:D01	CH21PRN
15764	377944	RTA22200262F.e.03.2.P.Seq	F	M00064328B:H04	CH22PRC
15765	745559	RTA22200262F.m.04.1.P.Seq	F	M00064359B:H12	CH22PRC
15766	818326	RTA22200265F.d.08.1.P.Seq	F	M00064524A:A09	CH22PRC
15767	379879	RTA22200264F.b.23.1.P.Seq	F	M00064446A:D11	CH22PRC
15768	819640	RTA22200257F.f.24.1.P.Seq	F	M00064165A:B12	CH21PRN
15769	818326	RTA22200265F.a.14.1.P.Seq	F	M00064514D:F11	CH22PRC
15770	243524	RTA22200265F.g.04.1.P.Seq	F	M00064532D:G06	CH22PRC
15771	43995	RTA22200261F.l.02.1.P.Seq	F	M00064294D:F01	CH22PRC
15772	597854	RTA22200262F.g.06.2.P.Seq	F	M00064337D:F01	CH22PRC
15773	268290	RTA22200260F.p.14.1.P.Seq	F	M00063981D:A06	CH22PRC
15774	818043	RTA22200256F.p.10.2.P.Seq	F	M00064138A:F11	CH21PRN
15775	830930	RTA22200267F.b.03.1.P.Seq	F	M00064652B:D09	CH22PRC
15776	389627	RTA22200260F.j.01.1.P.Seq	F	M00063957A:E02	CH22PRC
15777	378730	RTA22200260F.i.07.1.P.Seq	F	M00063955C:F07	CH22PRC
15778	819037	RTA22200260F.n.09.1.P.Seq	F	M00063972C:E10	CH22PRC
15779	830397	RTA22200261F.g.14.1.P.Seq	F	M00064005D:A08	CH22PRC
15780	450247	RTA22200261F.e.10.1.P.Seq	F	M00063998C:E09	CH22PRC
15781	819273	RTA22200252F.b.09.1.P.Seq	F	M00063517A:A04	CH21PRN
15782	587779	RTA22200257F.i.11.3.P.Seq	F	M00064175B:B09	CH21PRN
15783	818639	RTA22200256F.j.09.1.P.Seq	F	M00064115B:E12	CH21PRN
15784	615617	RTA22200261F.o.13.1.P.Seq	F	M00064309C:H09	CH22PRC
15785	79309	RTA22200257F.j.13.3.P.Seq	F	M00064180A:G03	CH21PRN
15786	748994	RTA22200261F.o.20.1.P.Seq	F	M00064310C:A10	CH22PRC
15787	818682	RTA22200258F.h.07.1.P.Seq	F	M00064271B:D03	CH21PRN
15788	373061	RTA22200253F.j.09.1.P.Seq	F	M00063795C:D09	CH21PRN
15789	484413	RTA22200253F.g.09.1.P.Seq	F	M00063781B:B10	CH21PRN

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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15791	569532	RTA22200252F.h.18.1.P.Seq	F	M00063613D:C11	CH21PRN
15792	170313	RTA22200255F.g.20.1.P.Seq	F	M00063949D:A05	CH21PRN
15793	818682	RTA22200253F.p.14.1.P.Seq	F	M00063841A:B09	CH21PRN
15794	377188	RTA22200255F.l.06.1.P.Seq	F	M00064043D:C09	CH21PRN
15795	518848	RTA22200257F.j.22.3.P.Seq	F	M00064186C:B03	CH21PRN
15796	45592	RTA22200259F.l.08.1.P.Seq	F	M00063557D:C07	CH22PRC
15797	819273	RTA22200255F.n.19.1.P.Seq	F	M00064053C:G04	CH21PRN
15798	397284	RTA22200251F.a.06.1.P.Seq	F	M00063151D:B10	CH21PRN
15799	818326	RTA22200258F.e.14.1.P.Seq	F	M00064260C:E05	CH21PRN
15800	819037	RTA22200251F.c.15.1.P.Seq	F	M00063452A:F08	CH21PRN
15801	817417	RTA22200253F.m.14.1.P.Seq	F	M00063818C:A09	CH21PRN
15802	819640	RTA22200254F.i.11.1.P.Seq	F	M00063891A:F11	CH21PRN
15803	818771	RTA22200254F.i.19.1.P.Seq	F	M00063892B:G02	CH21PRN
15804	389627	RTA22200254F.k.10.1.P.Seq	F	M00063898A:A10	CH21PRN
15805	379067	RTA22200260F.e.20.1.P.Seq	F	M00063593A:D03	CH22PRC
15806	818544	RTA22200251F.f.02.1.P.Seq	F	M00063463D:B05	CH21PRN
15807	819440	RTA22200251F.j.22.1.P.Seq	F	M00063485A:E05	CH21PRN
15808	817417	RTA22200251F.k.10.1.P.Seq	F	M00063487C:C02	CH21PRN
15809	385307	RTA22200262F.k.11.1.P.Seq	F	M00064352C:H01	CH22PRC
15810	611440	RTA22200263F.d.24.2.P.Seq	F	M00064386B:C02	CH22PRC
15811	376056	RTA22200259F.e.16.1.P.Seq	F	M00063538D:B01	CH22PRC
15812	611440	RTA22200263F.d.24.1.P.Seq	F	M00064386B:C02	CH22PRC
15813	820061	RTA22200264F.f.09.1.P.Seq	F	M00064457D:C09	CH22PRC
15814	617825	RTA22200264F.p.06.1.P.Seq	F	M00064508A:B09	CH22PRC
15815	819440	RTA22200257F.h.17.1.P.Seq	F	M00064173B:E01	CH21PRN
15816	819145	RTA22200266F.m.08.1.P.Seq	F	M00064631C:H11	CH22PRC
15817	817653	RTA22200265F.p.07.1.P.Seq	F	M00064579A:C06	CH22PRC
15818	611440	RTA22200263F.e.01.1.P.Seq	F	M00064386B:C02	CH22PRC
15819	375958	RTA22200264F.j.22.1.P.Seq	F	M00064476D:C04	CH22PRC
15820	611440	RTA22200257F.a.20.1.P.Seq	F	M00064144D:A07	CH21PRN
15821	831049	RTA22200266F.o.13.1.P.Seq	F	M00064637B:F03	CH22PRC
15822	818162	RTA22200266F.g.18.1.P.Seq	F	M00064610D:H01	CH22PRC
15823	553200	RTA22200263F.p.02.1.P.Seq	F	M00064429D:B07	CH22PRC
15824	139677	RTA22200254F.o.07.1.P.Seq	F	M00063910D:A12	CH21PRN
15825	139677	RTA22200252F.c.11.1.P.Seq	F	M00063520D:E11	CH21PRN
15826	397284	RTA22200262F.i.22.2.P.Seq	F	M00064346C:B09	CH22PRC
15827	385810	RTA22200256F.m.04.2.P.Seq	F	M00064126C:F12	CH21PRN
15828	404624	RTA22200261F.e.07.1.P.Seq	F	M00063997C:B12	CH22PRC
15829	375958	RTA22200262F.b.14.2.P.Seq	F	M00064322C:A10	CH22PRC
15830	616555	RTA22200265F.b.24.1.P.Seq	F	M00064520A:E04	CH22PRC

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
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15832	295694	RTA22200260F.o.20.1.P.Seq	F	M00063978B:B06	CH22PRC
15833	36113	RTA22200265F.e.06.1.P.Seq	F	M00064526D:F05	CH22PRC
15834	831812	RTA22200263F.f.05.1.P.Seq	F	M00064390A:C05	CH22PRC
15835	817653	RTA22200252F.g.23.1.P.Seq	F	M00063610D:C11	CH21PRN
15836	397284	RTA22200252F.m.15.1.P.Seq	F	M00063636A:E01	CH21PRN
15837	817979	RTA22200253F.p.15.1.P.Seq	F	M00063841A:E08	CH21PRN
15838	817653	RTA22200255F.m.18.1.P.Seq	F	M00064048C:G12	CH21PRN
15839	611440	RTA22200253F.f.03.1.P.Seq	F	M00063774A:D09	CH21PRN
15840	386014	RTA22200261F.f.06.1.P.Seq	F	M00064001A:B03	CH22PRC
15841	549981	RTA22200255F.b.10.1.P.Seq	F	M00063925B:F04	CH21PRN
15842	193373	RTA22200255F.l.21.1.P.Seq	F	M00064046A:G02	CH21PRN
15843	400619	RTA22200255F.g.14.1.P.Seq	F	M00063947D:D01	CH21PRN
15844	831149	RTA22200261F.o.21.1.P.Seq	F	M00064310D:F03	CH22PRC
15845	36113	RTA22200255F.d.16.1.P.Seq	F	M00063932D:G08	CH21PRN
15846	817503	RTA22200253F.l.16.1.P.Seq	F	M00063805D:E05	CH21PRN
15847	376588	RTA22200260F.i.11.1.P.Seq	F	M00063955D:F05	CH22PRC
15848	141079	RTA22200252F.f.23.1.P.Seq	F	M00063606C:B04	CH21PRN
15849	818063	RTA22200253F.p.04.1.P.Seq	F	M00063839A:F01	CH21PRN
15850	455264	RTA22200253F.n.14.1.P.Seq	F	M00063828A:H12	CH21PRN
15851	189234	RTA22200251F.f.17.1.P.Seq	F	M00063466C:C11	CH21PRN
15852	295694	RTA22200265F.j.05.1.P.Seq	F	M00064550A:A07	CH22PRC
15853	648679	RTA22200260F.f.06.1.P.Seq	F	M00063594B:H07	CH22PRC
15854	830930	RTA22200264F.e.10.1.P.Seq	F	M00064452D:E11	CH22PRC
15855	818497	RTA22200256F.d.07.1.P.Seq	F	M00064079C:A10	CH21PRN
15856	373928	RTA22200256F.d.19.1.P.Seq	F	M00064082A:A08	CH21PRN
15857	385307	RTA22200263F.j.12.1.P.Seq	F	M00064406B:H06	CH22PRC
15858	403453	RTA22200266F.e.10.1.P.Seq	F	M00064601D:B05	CH22PRC
15859	730318	RTA22200264F.c.09.1.P.Seq	F	M00064447B:A07	CH22PRC
15860	44183	RTA22200271F.a.01.1.P.Seq	F	M00021929A:D03	CH03MAH
15861	373928	RTA22200255F.d.22.1.P.Seq	F	M00063934B:E04	CH21PRN
15862	404624	RTA22200255F.d.23.1.P.Seq	F	M00063934C:C10	CH21PRN
15863	403173	RTA22200253F.a.21.1.P.Seq	F	M00063685A:C02	CH21PRN
15864	372700	RTA22200253F.c.06.1.P.Seq	F	M00063689D:E12	CH21PRN
15865	374343	RTA22200261F.h.04.1.P.Seq	F	M00064008A:B01	CH22PRC
15866	597854	RTA22200255F.j.03.1.P.Seq	F	M00064033D:B01	CH21PRN
15867	817417	RTA22200255F.a.23.1.P.Seq	F	M00063922B:A12	CH21PRN
15868	818497	RTA22200257F.k.05.3.P.Seq	F	M00064188B:G08	CH21PRN
15869	377696	RTA22200255F.f.15.1.P.Seq	F	M00063943B:G12	CH21PRN
15870	379105	RTA22200252F.n.19.1.P.Seq	F	M00063642B:A08	CH21PRN
15871	831188	RTA22200267F.o.02.1.P.Seq	F	M00064723D:H11	CH22PRC

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
15872	376056	RTA22200253F.m.09.1.P.Seq	F	M00063810C:E03	CH21PRN
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15874	376056	RTA22200254F.i.03.1.P.Seq	F	M00063890A:F11	CH21PRN
15875	831812	RTA22200266F.j.10.1.P.Seq	F	M00064620C:D01	CH22PRC
15876	141079	RTA22200260F.i.14.1.P.Seq	F	M00063956A:F05	CH22PRC
15877	19148	RTA22200265F.o.18.1.P.Seq	F	M00064577C:B12	CH22PRC
15878	124396	RTA22200252F.a.14.1.P.Seq	F	M00063514C:E08	CH21PRN
15879	831026	RTA22200265F.c.03.1.P.Seq	F	M00064520A:F08	CH22PRC
15880	819037	RTA22200263F.i.23.1.P.Seq	F	M00064405B:C04	CH22PRC
15881	380207	RTA22200263F.i.19.1.P.Seq	F	M00064404C:G05	CH22PRC
15882	819460	RTA22200255F.c.13.1.P.Seq	F	M00063928A:G09	CH21PRN
15883	379067	RTA22200253F.g.23.1.P.Seq	F	M00063784C:E10	CH21PRN
15884	403173	RTA22200252F.p.23.1.P.Seq	F	M00063682A:C04	CH21PRN
15885	3856	RTA22200269F.a.05.1.P.Seq	F	M00003773D:H02	CH01COH
15886	378551	RTA22200263F.d.17.1.P.Seq	F	M00064385D:C11	CH22PRC
15887	456089	RTA22200272F.a.09.1.P.Seq	F	M00043134A:A05	CH19COP
15888	549981	RTA22200267F.a.22.1.P.Seq	F	M00064650B:B07	CH22PRC
15889	378551	RTA22200265F.m.21.1.P.Seq	F	M00064568A:H06	CH22PRC
15890	819201	RTA22200256F.n.23.2.P.Seq	F	M00064132B:B07	CH21PRN
15891	374826	RTA22200251F.c.20.1.P.Seq	F	M00063453B:F08	CH21PRN
15892	389409	RTA22200253F.l.23.1.P.Seq	F	M00063807A:D12	CH21PRN
15893	819149	RTA22200260F.a.17.1.P.Seq	F	M00063575B:G02	CH22PRC
15894	389409	RTA22200255F.e.18.1.P.Seq	F	M00063939C:D06	CH21PRN
15895	818165	RTA22200254F.h.15.1.P.Seq	F	M00063888D:F02	CH21PRN
15896	817757	RTA22200252F.i.15.1.P.Seq	F	M00063617D:F09	CH21PRN
15897	553242	RTA22200263F.i.20.1.P.Seq	F	M00064404D:A06	CH22PRC
15898	385615	RTA22200265F.b.08.1.P.Seq	F	M00064517B:F10	CH22PRC
15899	819102	RTA22200258F.h.19.1.P.Seq	F	M00064272C:G01	CH21PRN
15900	817757	RTA22200255F.o.16.1.P.Seq	F	M00064057C:H10	CH21PRN
15901	385615	RTA22200265F.b.07.1.P.Seq	F	M00064517B:F04	CH22PRC
15902	385615	RTA22200253F.l.06.1.P.Seq	F	M00063804C:A11	CH21PRN
15903	827355	RTA22200266F.n.23.1.P.Seq	F	M00064636B:A04	CH22PRC
15904	817629	RTA22200259F.a.13.1.P.Seq	F	M00063165A:C09	CH22PRC
15905	817514	RTA22200260F.h.02.1.P.Seq	F	M00063600C:C09	CH22PRC
15906	817514	RTA22200252F.p.21.1.P.Seq	F	M00063681B:C02	CH21PRN
15907	680563	RTA22200265F.f.13.1.P.Seq	F	M00064530B:H02	CH22PRC
15908	827355	RTA22200255F.e.20.1.P.Seq	F	M00063939C:H01	CH21PRN
15909	377286	RTA22200254F.a.04.1.P.Seq	F	M00063843B:D07	CH21PRN
15910	680563	RTA22200258F.g.18.1.P.Seq	F	M00064268D:G03	CH21PRN
15911	819156	RTA22200255F.h.06.1.P.Seq	F	M00064021D:H01	CH21PRN
15912	220584	RTA22200261F.f.22.1.P.Seq	F	M00064003B:C10	CH22PRC

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
15913	616555	RTA22200263F.o.12.1.P.Seq	F	M00064428B:A12	CH22PRC
15914	819498	RTA22200254F.o.14.1.P.Seq	F	M00063912A:D06	CH21PRN
15915	817508	RTA22200257F.h.01.1.P.Seq	F	M00064171D:E05	CH21PRN
15916	817690	RTA22200257F.e.05.1.P.Seq	F	M00064159A:H03	CH21PRN
15917	819156	RTA22200256F.h.13.1.P.Seq	F	M00064106C:G03	CH21PRN
15918	830904	RTA22200266F.j.12.1.P.Seq	F	M00064620D:G05	CH22PRC
15919	819498	RTA22200253F.b.04.1.P.Seq	F	M00063686B:E07	CH21PRN
15920	817508	RTA22200257F.g.24.1.P.Seq	F	M00064171D:E05	CH21PRN
15921	817508	RTA22200252F.a.19.1.P.Seq	F	M00063515B:F06	CH21PRN
15922	831160	RTA22200267F.h.01.1.P.Seq	F	M00064690A:C04	CH22PRC
15923	817762	RTA22200252F.k.13.1.P.Seq	F	M00063627C:F06	CH21PRN
15924	377286	RTA22200266F.k.07.1.P.Seq	F	M00064624C:B03	CH22PRC
15925	831160	RTA22200267F.g.24.1.P.Seq	F	M00064690A:C04	CH22PRC
15926	819994	RTA22200256F.k.11.1.P.Seq	F	M00064119C:D12	CH21PRN
15927	819994	RTA22200256F.k.09.1.P.Seq	F	M00064119B:H10	CH21PRN
15928	373298	RTA22200259F.c.19.1.P.Seq	F	M00063533A:C12	CH22PRC
15929	819894	RTA22200256F.m.03.2.P.Seq	F	M00064126C:C02	CH21PRN
15930	372718	RTA22200260F.b.22.1.P.Seq	F	M00063580D:B06	CH22PRC
15931	827355	RTA22200262F.l.20.1.P.Seq	F	M00064358A:G03	CH22PRC
15932	819894	RTA22200255F.d.09.1.P.Seq	F	M00063931B:E10	CH21PRN
15933	827355	RTA22200266F.e.07.1.P.Seq	F	M00064601C:G07	CH22PRC
15934	372718	RTA22200256F.l.03.1.P.Seq	F	M00064122C:B06	CH21PRN
15935	647435	RTA22200251F.b.10.1.P.Seq	F	M00063156D:H10	CH21PRN
15936	450262	RTA22200265F.a.10.1.P.Seq	F	M00064514A:G10	CH22PRC
15937	484703	RTA22200255F.i.20.1.P.Seq	F	M00064032D:G04	CH21PRN
15938	819498	RTA22200256F.f.12.1.P.Seq	F	M00064089B:F09	CH21PRN
15939	406043	RTA22200263F.i.12.1.P.Seq	F	M00064404A:B05	CH22PRC
15940	817500	RTA22200255F.f.24.1.P.Seq	F	M00063945A:C03	CH21PRN
15941	818180	RTA22200264F.o.18.1.P.Seq	F	M00064506A:C07	CH22PRC
15942	818143	RTA22200251F.a.03.1.P.Seq	F	M00063151A:G06	CH21PRN
15943	819756	RTA22200267F.a.18.1.P.Seq	F	M00064649A:E04	CH22PRC
15944	406908	RTA22200257F.i.18.3.P.Seq	F	M00064176D:H10	CH21PRN
15945	124863	RTA22200256F.o.21.2.P.Seq	F	M00064136C:D12	CH21PRN
15946	429009	RTA22200257F.e.24.1.P.Seq	F	M00064161B:G04	CH21PRN
15947	402586	RTA22200257F.i.24.3.P.Seq	F	M00064178B:A05	CH21PRN
15948	400475	RTA22200254F.i.04.1.P.Seq	F	M00063890A:H04	CH21PRN
15949	403453	RTA22200264F.d.12.1.P.Seq	F	M00064450C:E07	CH22PRC
15950	383021	RTA22200259F.d.06.1.P.Seq	F	M00063534C:A02	CH22PRC
15951	394913	RTA22200254F.p.10.1.P.Seq	F	M00063915C:E01	CH21PRN
15952	831361	RTA22200263F.k.19.1.P.Seq	F	M00064414D:D06	CH22PRC
15953	646020	RTA22200267F.n.21.1.P.Seq	F	M00064723C:H04	CH22PRC

Table 120

SEQ ID	CLUSTER	SEQ NAME	ORIENT	CLONE ID	LIBRARY
15954	831361	RTA22200263F.l.03.1.P.Seq	F	M00064415B:G03	CH22PRC
15955	831580	RTA22200261F.f.18.1.P.Seq	F	M00064002C:H09	CH22PRC
15956	402586	RTA22200257F.j.01.3.P.Seq	F	M00064178B:A05	CH21PRN
15957	400475	RTA22200262F.j.21.1.P.Seq	F	M00064349D:H01	CH22PRC
15958	818937	RTA22200262F.h.14.2.P.Seq	F	M00064341A:C02	CH22PRC
15959	557697	RTA22200261F.j.20.1.P.Seq	F	M00064018C:E07	CH22PRC
15960	831361	RTA22200265F.m.24.1.P.Seq	F	M00064569B:A09	CH22PRC
15961	194490	RTA22200252F.c.10.1.P.Seq	F	M00063520D:D08	CH21PRN
15962	818143	RTA22200254F.b.18.1.P.Seq	F	M00063848C:G11	CH21PRN
15963	377286	RTA22200259F.a.10.1.P.Seq	F	M00063163A:G04	CH22PRC
15964	831361	RTA22200265F.n.01.1.P.Seq	F	M00064569B:A09	CH22PRC
15965	385307	RTA22200255F.p.07.1.P.Seq	F	M00064060B:D03	CH21PRN
15966	378447	RTA22200251F.c.01.1.P.Seq	F	M00063158A:E11	CH21PRN
15967	378447	RTA22200251F.b.24.1.P.Seq	F	M00063158A:E11	CH21PRN
15968	817514	RTA22200260F.m.17.1.P.Seq	F	M00063968D:G08	CH22PRC
15969	818942	RTA22200255F.f.03.1.P.Seq	F	M00063941B:C12	CH21PRN
15970	818942	RTA22200267F.e.23.1.P.Seq	F	M00064678D:F05	CH22PRC
15971	817363	RTA22200266F.f.04.1.P.Seq	F	M00064605C:G05	CH22PRC
15972	818942	RTA22200255F.i.02.1.P.Seq	F	M00064025D:E07	CH21PRN
15973	818942	RTA22200265F.g.23.1.P.Seq	F	M00064534D:F06	CH22PRC
15974	817457	RTA22200267F.e.15.1.P.Seq	F	M00064675C:E09	CH22PRC
15975	831968	RTA22200263F.f.23.1.P.Seq	F	M00064393B:H04	CH22PRC
15976	530941	RTA22200253F.h.05.1.P.Seq	F	M00063785C:F03	CH21PRN
15977	763446	RTA22200257F.j.05.3.P.Seq	F	M00064179A:C04	CH21PRN
15978	763446	RTA22200255F.n.21.1.P.Seq	F	M00064053D:F02	CH21PRN
15979	819219	RTA22200256F.f.16.1.P.Seq	F	M00064090C:A02	CH21PRN
15980	763446	RTA22200258F.b.19.2.P.Seq	F	M00064248A:E02	CH21PRN
15981	10154				
15982	10154				

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
SEQ ID	ACCESSION	DESCRIPTION	P VALUE	ACCESSION	DESCRIPTION	P VALUE
15685	<NONE>	<NONE>	<NONE>	1077580	hypothetical protein YDR125c - yeast	7
15686	<NONE>	<NONE>	<NONE>	4585925	(AC007211) unknown protein	6
15687	<NONE>	<NONE>	<NONE>	1085306	EVI1 protein - human	4.3
15688	<NONE>	<NONE>	<NONE>	3876587	(Z81521) predicted using Genefinder; cDNA EST yk233g4.5 comes from this gene; cDNA EST yk233g4.3 comes from this gene [Caenorhabditis elegans]	0.85
15689	<NONE>	<NONE>	<NONE>	1086591	(U41007) similar to S. cerevisiae nuclear protein SNF2	0.34
15690	<NONE>	<NONE>	<NONE>	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	0.29
15691	<NONE>	<NONE>	<NONE>	2633160	(Z99108) similar to surface adhesion YfiQ [Bacillus subtilis]	0.19
15692	<NONE>	<NONE>	<NONE>	755468	(U19879) transmembrane protein [Xenopus laevis]	0.042
15693	<NONE>	<NONE>	<NONE>	4507339	T brachyury (mouse) homolog protein [Homo sapiens]	0.029

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15694	<NONE>	<NONE>	<NONE>	729711	PROTEASE DEGS PRECURSOR 3.4.21.-) hhoB - Escherichia coli > gi 558913 (U15661) HhoB [Escherichia coli] > gi 606174 (U18997) ORF o355 coli] > gi 1789630 (AE000402) protease [Escherichia coli]	0.004
15695	<NONE>	<NONE>	<NONE>	3168911	(AF068718) No definition line found [Caenorhabditis elegans]	8e-013
15696	<NONE>	<NONE>	<NONE>	2832777	(AL021086) /prediction=(me thod;; comes from the 5' UTR [Drosophila melanogaster]	3e-040
15697	X78712	H.sapiens mRNA for glycerol kinase testis specific 2	2.1	2852449	(D88207) protein kinase [Arabidopsis thaliana] > gi 2947061 (AC002521) putative protein kinase	9.1
15698	X60760	L.esculentum TDR8 mRNA	2.1	157272	(L11345) DNA- binding protein [Drosophila melanogaster]	5
15699	U40853	Oryctolagus cuniculus pulmonary surfactant protein B (SP-B) gene, complete cds	2	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15700	AF083655	Homo sapiens procollagen C-proteinase enhancer protein (PCOLCE) gene, 5' flanking region and complete cds	2	<NONE>	<NONE>	<NONE>
15701	AJ223776	Staphylococcus warneri hld gene	2	<NONE>	<NONE>	<NONE>
15702	U40853	Oryctolagus cuniculus pulmonary surfactant protein B (SP-B) gene, complete cds	2	<NONE>	<NONE>	<NONE>
15703	X04436	Clostridium tetani gene for tetanus toxin	2	<NONE>	<NONE>	<NONE>
15704	Z35787	S.cerevisiae chromosome II reading frame ORF YBL026w	2	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	8.4
15705	X78712	H.sapiens mRNA for glycerol kinase testis specific 2	2	2852449	(D88207) protein kinase [Arabidopsis thaliana] > gi 2947061 (AC002521) putative protein kinase	8.2
15706	Z15056	B.subtilis genes spoVD, murE, mraY, murD	2	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	2.8

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15707	S65623	cAMP-regulated enhancer-binding protein 1 of 3]	2	119266	PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT I-BINDING ACTIVITY) regulatory protein elf-1 - fruit fly (Drosophila melanogaster) > gi 7939 emb CAA33692 (X15657) Elf-1 protein (AA 1-1063) [Drosophila melanogaster]	0.55
15708	NM_004415.1	Homo sapiens desmoplakin (DPI; DPII) (DSP) mRNA, complete cds	2	2649177	(AE001008) conserved hypothetical protein [Archaeoglobus fulgidus]	0.2
15709	AF031552	Vibrio cholerae magnesium transporter (mgtE) gene, partial cds; sensor kinase (vieS), response regulator (vieA), and response regulator (vieB) genes, complete cds; and collagenase (vcc) gene, partial cds	2	2088714	(AF003139) strong similarity to NADPH oxidases; partial CDS, the gene begins in the neighboring clone	2e-013
15710	AF116852.1	Danio rerio dickkopf-1 (dkk1) mRNA, complete cds	2	3800951	(AF100657) No definition line found [Caenorhabditis elegans] -	2e-019
15711	X82595	P.sativum fuc gene	1.9	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15712	AF008216	Homo sapiens candidate tumor suppressor pp32r1	1.9	<NONE>	<NONE>	<NONE>
15713	AF130672.1	Felis catus clone Fca603 microsatellite sequence	1.9	<NONE>	<NONE>	<NONE>
15714	AJ007044	Oryctolagus Cuniculus sod gene	1.9	388055	(L22981) merozoite surface protein-1 [Plasmodium chabaudi]	7.8
15715	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	1.9	160925	(M94346) A.1.12/9 antigen [Schistosoma mansoni]	7.7
15716	U30290	Rattus norvegicus galanin receptor GALR1 mRNA, complete cds	1.9	3024079	GALECTIN-4 (LACTOSE-BINDING LECTIN 4) (L-36 LACTOSE BINDING PROTEIN) (L36LBP) > gi 2281707 sapiens] > gi 2623387 (U82953) galectin-4 [Homo sapiens]	4.5
15717	Y13234	Chironomus tentans mRNA for chitinase, 1695 bp	1.9	4567068	(AF125568) tumor suppressing STF cDNA 4 [Homo sapiens]	3.4
15718	NM_003644.1	Homo sapiens growth arrest-specific 7 (GAS7) mRNA > :: emb AJ224876 HSAJ4876 Homo sapiens mRNA for GAS7 protein	1.9	125560	PROTEIN KINASE C, GAMMA TYPE C (EC 2.7.1.-) gamma - rabbit > gi 165652 (M19338) protein kinase delta [Oryctolagus cuniculus]	0.53

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15719	AB013448.1	Oryza sativa gene for Pib, complete cds	1.8	<NONE>	<NONE>	<NONE>
15720	D63854	Human cytomegalovirus DNA, replication origin	1.8	<NONE>	<NONE>	<NONE>
15721	AB002340	Human mRNA for KIAA0342 gene, complete cds	1.8	<NONE>	<NONE>	<NONE>
15722	AF017779	Mus musculus vitamin D receptor gene, promoter region	1.8	<NONE>	<NONE>	<NONE>
15723	D63854	Human cytomegalovirus DNA, replication origin	1.8	<NONE>	<NONE>	<NONE>
15724	M24102	Bovine ADP/ATP translocase T1 mRNA, complete cds.	1.8	<NONE>	<NONE>	<NONE>
15725	AC004497	Homo sapiens chromosome 21, P1 clone LBNL#6	1.8	<NONE>	<NONE>	<NONE>
15726	M37394	Rat epidermal growth factor receptor mRNA.	1.8	<NONE>	<NONE>	<NONE>
15727	AF006304	Saccharomyces cerevisiae protein tyrosine phosphatase (PTP3) gene, complete cds	1.8	<NONE>	<NONE>	<NONE>
15728	D13454	Candida albicans CACHS3 gene for chitin synthase III	1.8	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15729	Y00354	Xenopus laevis gene encoding vitellogenin A2	1.8	1077580	hypothetical protein YDR125c - yeast	7.5
15730	U90936	Aspergillus niger px27 gene, promoter region	1.8	4337033	(AF124138) transcriptional activator protein CdaR [Streptomyces coelicolor] transcriptional regulator [Streptomyces coelicolor]	7.3
15731	D84448	Cavia cobaya mRNA for Na ⁺ , K ⁺ -ATPase beta-3 subunit, complete cds	1.8	4704603	(AF109916) putative dehydrin	7.1
15732	AF039948	Xenopus laevis clone H-0 transcription elongation factor S-II (TFIIS) precursor RNA, isoform TFIIS.h, partial cds	1.8	1695839	(U58151) envelope glycoprotein [Human immunodeficiency virus type 1]	5.6
15733	M18061	Xenopus laevis vitellogenin gene, complete cds.	1.8	780502	(U18466) AP endonuclease class II [African swine fever virus] >gi 1097525 p rf 2113434ET AP endonuclease:IS OTYPE=class II [African swine fever virus]	3.1
15734	U61112	Mus musculus Eya3 homolog mRNA, complete cds	1.8	3043646	(AB011133) KIAA0561 protein [Homo sapiens]	1.9

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15735	AB018442	Oryza sativa mRNA for phytochrome C, complete cds	1.8	4455041	(AF116463) unknown [Streptomyces lincolnensis]	0.49
15736	D63854	Human cytomegalovirus DNA, replication origin	1.8	1169200	DNA-DAMAGE-REPAIR/TOLE RATION PROTEIN DRT111 PRECURSOR >gi 421829 pir S33706 DNA-damage resistance protein - Arabidopsis thaliana and DNA-damage resistance protein (DRT111) mRNA, complete cds.], gene product [Arabidopsis thaliana]	0.22
15737	D26549	Bovine mRNA for adseverin, complete cds	1.8	755468	(U19879) transmembrane protein [Xenopus laevis]	0.042
15738	J05211	Human desmoplakin mRNA, 3' end.	1.8	728867	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR >gi 99694 pir S21961 proline-rich protein APG - Arabidopsis thaliana >gi 22599 emb CAA42925	0.015

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15739	NM_004415.1	Homo sapiens desmoplakin (DPI, DPII) (DSP) mRNA, complete cds	1.8	728867	ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR > gi 99694 pir S21961 proline-rich protein APG - Arabidopsis thaliana > gi 22599 emb CAA42925	0.015
15740	AF038604	Caenorhabditis elegans cosmid B0546	1.8	3877951	(Z81555) predicted using Genefinder	3e-008
15741	AF038604	Caenorhabditis elegans cosmid B0546	1.8	3877951	(Z81555) predicted using Genefinder	2e-011
15742	U23551	Prochlorothrix hollandica phosphomannomutase	1.8	2828280	(AL021687) putative protein [Arabidopsis thaliana] > gi 2832633 emb CAA16762 (AL021711) putative protein [Arabidopsis thaliana]	2e-013
15743	S60150	ORF1...ORF6 {3' terminal reigon} [chrysanthemum virus B CVB, Genomic RNA, 6 genes, 3426 nt]	1.8	1065454	(U40410) C54G7.2 gene product [Caenorhabditis elegans]	2e-019
15744	AB014558	Homo sapiens mRNA for KIAA0658 protein, partial cds	1.8	3850072	(AL033385) dna-directed rna polymerase iii subunit [Schizosaccharomyces pombe]	6e-027

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15745	X17191	E.gracilis chloroplast RNA polymerase rpoB-rpoC1-rpoC2 operon	1.7	<NONE>	<NONE>	<NONE>
15746	X07729	R.norvegicus gene encoding neuron-specific enolase, exons 8-12	1.7	4584544	(AL049608) extensin-like protein	8.8
15747	D38178	Human gene for cytosolic phospholipase A2, exon 1	1.7	73714	infected cell protein ICP34.5 - human herpesvirus 1 (strain F) > gi 330123 (M12240) infected cell protein [Herpes simplex virus type 1]	1.1
15748	U23551	Prochlorothrix hollandica phosphomannomutase	1.7	2828280	(AL021687) putative protein [Arabidopsis thaliana] > gi 2832633 emb CAA16762 (AL021711) putative protein [Arabidopsis thaliana]	2e-010
15749	Y00525	Klebsiella pneumoniae nifL gene for regulatory protein	1.6	3800951	(AF100657) No definition line found [Caenorhabditis elegans]	6e-013
15750	AF100170.1	Bos taurus major fibrous sheath protein precursor, mRNA, complete cds	1.5	463552	(U05877) AF-1 [Homo sapiens]	0.074
15751	Y13441	Homo sapiens Rox gene, exon 2	0.74	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15752	L46792	Actinidia deliciosa clone AdXET-5 xyloglucan endotransglycosylase precursor (XET) mRNA, complete cds	0.73	3170252	(AF043636) circumsporozoite protein [Plasmodium chabaudi]	0.001
15753	U73489	Drosophila melanogaster Nem (nem) mRNA, complete cds	0.7	3915994	HYPOTHETICAL 53.2 KD PROTEIN IN PRC-PRPA INTERGENIC REGION	3e-005
15754	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.68	157272	(L11345) DNA-binding protein [Drosophila melanogaster]	8.5
15755	AF082012	Caenorhabditis elegans UDP-N-acetylglucosaminase: α -3-D-mannoside b-1,2-N-acetylglucosaminyltransferase I (gly-14) mRNA, complete cds	0.67	2494313	PUTATIVE TRANSLATION INITIATION FACTOR EIF-2B SUBUNIT 1 (EIF-2B GDP-GTP EXCHANGE FACTOR) eIF-2B, subunit alpha - Methanococcus jannaschii aIF-2B, subunit delta (aIF2BD) [Methanococcus jannaschii]	8.4
15756	U04354	Mus musculus ADSEVERIN mRNA, complete cds	0.67	4755188	(AC007018) unknown protein	8e-026

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15757	M68881	S.pombe cigl+ gene, complete cds.	0.67	2078441	(U56964) weak similarity to S. cerevisiae intracellular protein transport protein US)1 (SP:P25386)	2e-030
15758	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.66	2829685	PROTEIN-TYROSINE PHOSPHATAS E X PRECURSOR (R-PTP-X) (PTP IA-2BETA) (PROTEIN TYROSINE PHOSPHATAS E-NP) (PTP-NP) > gi 1515425 (U57345) protein tyrosine phosphatase-NP [Mus musculus]	6.2
15759	Z15056	B.subtilis genes spoVD, murE, mraY, murD	0.66	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	2.1
15760	M86808	Human pyruvate dehydrogenase complex (PDHA2) gene, complete cds.	0.65	<NONE>	<NONE>	<NONE>
15761	J03754	Rat plasma membrane Ca2+ ATPase-isoform 2 mRNA, complete cds.	0.65	4507549	transmembrane protein with EGF-like and two follistatin-like domains 1 > gi 755466	8e-006

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15762	NM_000887.1	Homo sapiens integrin, alpha X (antigen CD11C emb Y00093 H SP15095 H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.64	<NONE>	<NONE>	<NONE>
15763	L27080	Human melanocortin 5 receptor (MC5R) gene, complete cds.	0.64	<NONE>	<NONE>	<NONE>
15764	U07890	Mus musculus C57BL/6J epidermal surface antigen (mesa) mRNA, complete cds.	0.64	<NONE>	<NONE>	<NONE>
15765	AF079139	Streptomyces venezuelae pikCD operon, complete sequence	0.64	3041869	(U96109) proline-rich transcription factor ALX3 [Mus musculus]	2.8
15766	M16140	Chicken ovoinhibitor gene, exon 15.	0.64	123984	ACROSIN INHIBITORS IIA AND IIB	4e-008
15767	NM_000887.1	Homo sapiens integrin, alpha X (antigen CD11C emb Y00093 H SP15095 H.sapiens mRNA for leukocyte adhesion glycoprotein p150,95	0.63	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15768	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.63	<NONE>	<NONE>	<NONE>
15769	Z25470	H.sapiens melanocortin 5 receptor gene, complete CDS	0.63	<NONE>	<NONE>	<NONE>
15770	L19954	Bacillus subtilis feuA, B, and C genes, 3 ORFs, 2 complete cds's and 5'end.	0.63	<NONE>	<NONE>	<NONE>
15771	U44405	Spiroplasma citri chromosome pre-inversion border, SPV1-like sequences, transposase gene, partial cds, adhesin-like protein P58 gene, complete cds.	0.63	2499642	SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG > gi 1737181 (U73457) Cst20p [Candida albicans]	7.7
15772	Z28264	S.cerevisiae chromosome XI reading frame ORF YKR039w	0.63	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T00805 ...	2e-014

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15773	AE001107	Archaeoglobus fulgidus section 172 of 172 of the complete genome	0.62	<NONE>	<NONE>	<NONE>
15774	Z14112	B.firmus TopA gene encoding DNA topoisomerase I	0.62	310115	(L02530) Drosophila polarity gene (frizzled) homologue	0.026
15775	AF118101	Toxoplasma gondii protein kinase 6 (tpk6) mRNA, complete cds	0.62	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	4e-018
15776	M59743	Rabbit cardiac muscle Ca-2+ release channel	0.61	<NONE>	<NONE>	<NONE>
15777	M12036	Human tyrosine kinase-type receptor (HER2) gene, partial cds.	0.61	61962	(X58484) gag [Simian foamy virus]	7.5
15778	AF043195	Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A	0.61	1572629	(U69699) unknown protein precursor [Mus musculus]	7.5
15779	U18178	Human HLA class I genomic survey sequence.	0.61	1336688	(S81116) properdin [guinea pigs, spleen, Peptide, 470 aa] [Cavia]	5.7
15780	U44405	Spiroplasma citri chromosome pre-inversion border, SPV1-like sequences, transposase gene, partial cds, adhesin-like protein P58 gene, complete cds.	0.61	2827531	(AL021633) hypothetical protein	3.3

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15781	Z33011	M.capricolum DNA for CONTIG MC008	0.61	3915729	HYPERPLASTI C DISCS PROTEIN (HYD PROTEIN) > gi 2673887 (L14644) hyperplastic discs protein	0.26
15782	NM_001429 .1	Homo sapiens E1A binding protein p300 mRNA, complete cds. > :: gb 162297 1622 97 Sequence 1 from patent US 5658784	0.61	4204294	(AC003027) lcl prt_seq No definition line found	5e-005
15783	Z25418	C.familiaris MHC class Ib gene (DLA-79) gene, complete CDS	0.61	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	1e-007

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15784	AB002150	Bacillus subtilis DNA for FeuB, FeuA, YbbB, YbbC, YbbD, YbzA, YbbE, YbbF, YbbH, YbbI, YbbJ, YbbK, YbbL, YbbM, YbbP, complete cds	0.6	<NONE>	<NONE>	<NONE>
15785	Y07786	V.cholerae ORF's involved in lipopolysaccharide synthase	0.6	<NONE>	<NONE>	<NONE>
15786	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.6	<NONE>	<NONE>	<NONE>
15787	Z71403	S.cerevisiae chromosome XIV reading frame ORF YNL127w	0.6	<NONE>	<NONE>	<NONE>
15788	L34641	Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exon 10.	0.6	1147634	(U42213) micronemal TRAP-C1 protein homolog	9.6

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15789	AF070572	Homo sapiens clone 24778 unknown mRNA	0.6	399034	N-ACETYLMURAMOYL-L-ALANINE AMIDASE AMIB PRECURSOR > gi 628763 pir S41741 N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) - Escherichia coli > gi 304914 (L19346) N-acetylmuramoyl-L-alanine amidase [Escherichia coli] N-acetylmuramoyl-l-alanine amidase II; a	2.5
15790	X75627	C.burnetii trxB, spoIIIE and serS genes	0.6	3036833	(AJ003163) apsB [Emericella nidulans]	0.28
15791	Z99765	Flaveria pringlei gdcsh gene	0.59	<NONE>	<NONE>	<NONE>
15792	U02538	Mycoplasma hyopneumoniae J ATCC 25934 23S rRNA gene, partial sequence	0.59	<NONE>	<NONE>	<NONE>
15793	Z71403	S.cerevisiae chromosome XIV reading frame ORF YNL127w	0.59	<NONE>	<NONE>	<NONE>
15794	X03942	Mouse simple repetitive DNA (sqr family) transcript (clone pm1c 2) with conserved GACA/GATA repeats	0.59	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15795	U11844	Mus musculus glucose transporter (GLUT3) gene, exon 1	0.59	<NONE>	<NONE>	<NONE>
15796	D63395	Homo sapiens mRNA for NOTCH4, partial cds	0.59	4433616	(AF107018) alpha-mannosidase IIx [Mus musculus]	1.8
15797	Z33011	M. capricolum DNA for CONTIG MC008	0.59	3915729	HYPERPLASTIC DISCS PROTEIN (HYD PROTEIN) > gi 2673887 (L14644) hyperplastic discs protein	0.27
15798	U05670	Haemophilus influenzae DL42 Lex2A and Lex2B genes, complete cds.	0.58	<NONE>	<NONE>	<NONE>
15799	L27080	Human melanocortin 5 receptor (MC5R) gene, complete cds.	0.58	123984	ACROSIN INHIBITORS IIA AND IIB	2e-006
15800	AF043195	Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A	0.57	1572629	(U69699) unknown protein precursor [Mus musculus]	6.7
15801	U57707	Bos taurus activin receptor type IIB precursor	0.57	807646	(M17294) unknown protein [Human herpesvirus 4]	0.068
15802	Z17316	Kluyveromyces lactis for gene encoding phosphofructokinase beta subunit	0.56	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15803	M21535	Human erg protein (ets-related gene) mRNA, complete cds.	0.56	<NONE>	<NONE>	<NONE>
15804	M64932	Candida maltosa cyclohexamide resistance protein	0.56	3219524	(AF069428) NADH dehydrogenase subunit IV [Alligator mississippiensis] > gi 3367630 emb CAA73570 (Y13113) NADH dehydrogenase subunit 4 [Alligator mississippiensis]	1.3
15805	AE000342	Escherichia coli K-12 MG1655 section 232 of 400 of the complete genome	0.56	3874685	(Z78539) Similarity to S.pombe hypothetical protein C4G8.04 (SW:YAD4 SC HPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come...	0.088
15806	Z15056	B.subtilis genes spoVD, murE, mraY, murD	0.55	477124	P3A2 DNA binding protein homolog EWG - fruit fly (Drosophila melanogaster)	3.7

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15807	Z58167	H.sapiens CpG island DNA genomic MseI fragment, clone 30e10, forward read cpg30e10.ft1b	0.53	<NONE>	<NONE>	<NONE>
15808	M27159	Rat potassium channel-Kv2 gene, partial cds.	0.53	1850920	(U21247) Bet [Human spumaretrovirus]	0.9
15809	M15555	Mouse Ig germline V-kappa-24 chain (VK24C) gene, exons 1 and 2.	0.24	<NONE>	<NONE>	<NONE>
15810	U95097	Xenopus laevis mitotic phosphoprotein 43 mRNA, partial cds	0.24	399109	TRANSCRIPTI ON FACTOR BF-1 (BRAIN FACTOR 1) (BF1) > gi 92020 pir JH0672 brain factor 1 protein - rat > gi 203135 (M87634) BF-1 [Rattus norvegicus]	4
15811	AJ002014	Crythecodium cohnii mRNA for nuclear protein JUS1	0.24	416704	BALBIANI RING PROTEIN 3 PRECURSOR balbiani ring 3 (BR3) [Chironomus tentans]	0.36
15812	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.23	1388158	(U58204) myomesin [Gallus gallus]	8.8

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15813	NM_001432.1	Homo sapiens epiregulin (EREG) mRNA > :: dbj D30783 D30783 Homo sapiens mRNA for epiregulin, complete cds	0.23	2851520	TRANSFORMING GROWTH FACTOR ALPHA PRECURSOR (TGF-ALPHA) (EGF-LIKE TGF) (ETGF) (TGF TYPE 1) precursor - rat > gi 207282 (M31076) transforming growth factor alpha precursor [Rattus norvegicus]	2e-008
15814	U57043	Cebus apella gamma globin (gamma1) gene, complete cds	0.22	<NONE>	<NONE>	<NONE>
15815	AB023188.1	Homo sapiens mRNA for KIAA0971 protein, complete cds	0.22	<NONE>	<NONE>	<NONE>
15816	M18105	Yeast (S.cerevisiae) SST2 gene encoding desensitization to alpha- factor pheromone, complete cds.	0.22	<NONE>	<NONE>	<NONE>
15817	AJ001113	Homo sapiens UBE3A gene, exon 16	0.22	3122961	ENHANCER OF SPLIT GROUCHO-LIKE PROTEIN 1 > gi 2408145 (U18775) enhancer of split groucho	8.5

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15818	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.22	1388158	(U58204) myomesin [Gallus gallus]	8.1
15819	D42042	Human mRNA for KIAA0085 gene, partial cds	0.22	4827063	zinc finger protein 142 (clone pHZ-49) > gi 3123312 sp P52746 Z142 HUMAN ZINC FINGER PROTEIN 142 (KIAA0236) (HA4654) > gi 1510147 dbj BAA13242	6.1
15820	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.22	2853301	(AF007194) mucin [Homo sapiens]	1.6
15821	Z11653	H.sapiens DBH gene complex repeat polymorphism DNA	0.22	3819705	(AL032824) syntaxin binding protein 1; sec1 family secretory protein [Schizosaccharomyces pombe]	1.2
15822	L29063	Candida albicans fatty acid synthase alpha subunit (FAS2) gene, complete cds.	0.22	3046871	(AB003753) high sulfur protein B2E [Rattus norvegicus]	0.32
15823	M64865	Horse alcohol dehydrogenase-S-isoenzyme mRNA, complete cds.	0.22	2213909	(AF004874) latent TGF-beta binding protein-2 [Mus musculus]	0.037
15824	Y09472	B.taurus gene encoding preprododecapeptide	0.21	2909874	(AF047829) melatonin-related receptor [Ovis aries]	7.6

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15825	Y09472	B.taurus gene encoding preprododecapeptide	0.21	2909874	(AF047829) melatonin-related receptor [Ovis aries]	7.5
15826	X80301	N.tabacum axi 1 gene	0.21	2832715	(AJ003066) subunit beta of the mitochondrial fatty acid beta-oxidation multienzyme complex [Bos taurus]	6
15827	AF073485	Homo sapiens MHC class I-related protein MR1 precursor (MR1) gene, partial cds	0.21	2224559	(AB002307) KIAA0309 [Homo sapiens]	3.3
15828	S78251	growth hormone receptor {alternatively spliced, exon 1B} [sheep, Merino, skeletal muscle, mRNA Partial, 438 nt]	0.21	729381	DYNAMIN-1 (DYNAMIN BREDNM19)	2
15829	U16135	Synechococcus sp. Clp protease proteolytic subunit	0.21	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA 11) - rabbit	0.02
15830	X95601	M.hominis Imp3 and Imp4 genes	0.21	2995445	(Y10496) CDV-1 protein [Mus musculus]	0.005
15831	X95601	M.hominis Imp3 and Imp4 genes	0.21	2995447	(Y10495) CDV-1R protein [Mus musculus]	0.005

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15832	AF124249.1	Homo sapiens SH2-containing protein Nsp1 mRNA, complete cds	0.21	423456	epidermal growth factor-receptor-binding protein GRB-4 - mouse (fragment)	8e-010
15833	AF030282	Danio rerio homeobox protein Six7 (six7) mRNA, complete cds	0.21	3928083	(AC005770) unknown protein [Arabidopsis thaliana]	2e-014
15834	X83427	O.anatinus mitochondrial DNA, complete genome	0.21	132575	RIBONUCLEASE INHIBITOR	3e-021
15835	AJ001113	Homo sapiens UBE3A gene, exon 16	0.2	<NONE>	<NONE>	<NONE>
15836	AF081533.1	Anopheles gambiae putative gram negative bacteria binding protein gene, complete cds	0.2	<NONE>	<NONE>	<NONE>
15837	U70316	Dictyostelium discoideum IonA (iona) gene, partial cds	0.2	<NONE>	<NONE>	<NONE>
15838	AF009341	Homo sapiens E6-AP ubiquitin-protein ligase	0.2	<NONE>	<NONE>	<NONE>
15839	L35330	Rattus norvegicus glutathione S-transferase Yb3 subunit gene, complete cds.	0.2	3702275	(AC005793) KIAA0561 protein [AA 1-593] [Homo sapiens]	2.5
15840	AE000573.1	Helicobacter pylori 26695 section 51 of 134 of the complete genome	0.2	3947855	(AL034381) putative Golgi membrane protein	2.5

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15841	X83230	G.gallus hsp90beta gene	0.2	3258596	(U95821) putative transmembrane GTPase [Drosophila melanogaster]	0.81
15842	X57157	Chicken mRNA for Hsp47, heat shock protein 47	0.2	108325	insulin-like growth factor-binding protein 6	0.17
15843	M58748	Chicken alpha-globin gene domain with structural matrix attachment sites.	0.2	1086863	(U41272) T03G11.6 gene product [Caenorhabditis elegans]	4e-005
15844	AB016815	Anthocidaris crassispina mRNA for Src-type protein tyrosine kinase, complete cds	0.2	423456	epidermal growth factor-receptor-binding protein GRB-4 - mouse (fragment)	1e-012
15845	AF030282	Danio rerio homeobox protein Six7 (six7) mRNA, complete cds	0.2	3928083	(AC005770) unknown protein [Arabidopsis thaliana]	3e-014
15846	AL035559	Streptomyces coelicolor cosmid 9F2	0.2	2088714	(AF003139) strong similarity to NADPH oxidases; partial CDS, the gene begins in the neighboring clone	3e-022
15847	S79641	SDH = succinate dehydrogenase flavoprotein subunit Mutant, 387 nt]	0.2	4755188	(AC007018) unknown protein	2e-022
15848	X75383	H.sapiens mRNA for TFIIA-alpha	0.19	<NONE>	<NONE>	<NONE>

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15849	U53901	Hippopotamus amphibius b-casein gene, exon 7, partial cds	0.19	<NONE>	<NONE>	<NONE>
15850	J05265	Mouse interferon gamma receptor mRNA, complete cds.	0.19	77356	hypothetical 70K protein - eggplant mosaic virus	0.0005
15851	U72353	Rattus norvegicus lamin B1 mRNA, complete cds	0.19	3880857	(AL031633) cDNA EST yk404d1.5 comes from this gene; cDNA EST yk404d1.3 comes from this gene	2e-006
15852	AB016815	Anthocidaris crassispina mRNA for Src-type protein tyrosine kinase, complete cds	0.19	3930217	(AF047487) Nck-2 [Homo sapiens]	2e-007
15853	D10911	Mus musculus DNA for MS2 protein, complete cds	0.19	2662366	(D86332) membrane type-2 matrix metalloproteinase [Mus musculus]	5e-011
15854	AB015345	Homo sapiens HRIHFB2216 mRNA, partial cds	0.075	3877417	(Z66564) similar to anion exchange protein	6.4
15855	AF086410	Homo sapiens full length insert cDNA clone. ZD77B03	0.075	3023371	PHEROMONE B BETA 1 RECEPTOR	4.9
15856	K02024	Human T-cell lymphotropic virus type II env gene encoding envelope glycoprotein, complete cds.	0.075	2791527	(AL021246) PE_PGRS [Mycobacterium tuberculosis]	0.11

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15857	M10188	X.laevis mitochondrial DNA containing the D-loop, and the 12S rRNA, apocytochrome b, Glu-tRNA, Thr-tRNA, Pro-tRNA and Phe-tRNA genes.	0.074	4753163	huntingtin DISEASE PROTEIN) (HD PROTEIN) > gi 454415 (L12392) Huntington's Disease protein [Homo sapiens]	2.8
15858	X85525	G.gallus AG repeat region (GgaMU130)	0.073	984339	(U20966) Rev [Simian immunodeficiency virus]	3.6
15859	AJ238394.1	Homo sapiens AML2 gene (partial)	0.07	4240219	(AB020672) KIAA0865 protein [Homo sapiens]	2
15860	AF039704	Homo sapiens lysosomal pepstatin insensitive protease (CLN2) gene, complete cds	0.069	2894106	(Z78279) Collagen alpha1 [Rattus norvegicus]	0.39
15861	K02024	Human T-cell lymphotropic virus type II env gene encoding envelope glycoprotein, complete cds.	0.068	4504857	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 3 > gi 3309531 (AF031815) calcium-activated potassium channel [Homo sapiens]	0.5

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15862	Z60719	H.sapiens CpG island DNA genomic MseI fragment, clone 33a11, forward read cpg33a11.ft1m	0.068	4826874	nucleoporin 214kD (CAIN) PROTEIN NUP214 (NUCLEOPORIN NUP214) (214 KD NUCLEOPORIN) transforming protein (can) - human sapiens]	0.044
15863	AF053994	Lycopersicon esculentum Hcr2-0A (Hcr2-0A) gene, complete cds	0.068	2842699	PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE)	9e-009
15864	AJ233650.1	Equus caballus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Horsel	0.067	<NONE>	<NONE>	<NONE>
15865	M10188	X.laevis mitochondrial DNA containing the D-loop, and the 12S rRNA, apocytochrome b, Glu-tRNA, Thr-tRNA, Pro-tRNA and Phe-tRNA genes.	0.067	4753163	huntingtin DISEASE PROTEIN) (HD PROTEIN) > gi 454415 (L12392) Huntington's Disease protein [Homo sapiens]	2.5

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15866	U14646	Murine hepatitis virus Y strain S glycoprotein gene, complete cds.	0.067	3880930	(AL021481) similar to Phosphoglucomutase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T00805 ...	1e-019
15867	X15373	Mouse cerebellum mRNA for P400 protein	0.066	164507	(M81771) immunoglobulin gamma-chain [Sus scrofa]	9.4
15868	AF086410	Homo sapiens full length insert cDNA clone ZD77B03	0.066	3023371	PHEROMONE B BETA 1 RECEPTOR	4.2
15869	AL034492	Streptomyces coelicolor cosmid 6C5	0.066	3800951	(AF100657) No definition line found [Caenorhabditis elegans]	3e-015
15870	L13377	Staphylococcus aureus enterotoxin gene, 3' end.	0.065	<NONE>	<NONE>	<NONE>
15871	U83478	Thelephoraceae sp. 'Taylor #13' ITS1, 5.8S ribosomal RNA gene, and ITS2, complete sequence	0.065	3877335	(Z92786) predicted using Genefinder	9.1

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15872	AJ002014	Crythecodinium cohnii mRNA for nuclear protein JUS1	0.065	1213283	(U40576) SIM2 [Mus musculus]	0.47
15873	AB016804	Aloe arborescens mRNA for NADP-malic enzyme, complete cds	0.065	2832777	(AL021086) /prediction=(method;; comes from the 5' UTR [Drosophila melanogaster]	5e-036
15874	AJ002014	Crythecodinium cohnii mRNA for nuclear protein JUS1	0.063	1213283	(U40576) SIM2 [Mus musculus]	0.45
15875	AB023143.1	Homo sapiens mRNA for KIAA0926 protein, complete cds	0.024	132575	RIBONUCLEASE INHIBITOR	8e-026
15876	U72966	Human hepatocyte nuclear factor 4-alpha gene, exon 7	0.022	<NONE>	<NONE>	<NONE>
15877	X02801	Mouse gene for glial fibrillary acidic protein	0.022	2231607	(U85917) nef protein [Human immunodeficiency virus type 1]	7
15878	AF017636	Mesocricetus auratus 3-keto-steroid reductase	0.022	2723362	(AF023459) lustrin A [Haliotis rufescens]	0.097
15879	Z36879	F.pringlei gdcSP gene for P-protein of the glycine cleavage system	0.008	<NONE>	<NONE>	<NONE>
15880	X73150	P.sativum GapC1 gene	0.008	1572629	(U69699) unknown protein precursor [Mus musculus]	8.6
15881	AJ239031.1	Homo sapiens LSS gene, partial, exons 22, 23 and joined CDS	0.008	4508019	zinc finger protein 231 protein [Homo sapiens]	0.01

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15882	U76602	Human 180 kDa bullous pemphigoid antigen 2/type XVII collagen (BPAG2/COL17A1) gene, exons 49, 50, 51 and 52	0.007	3170252	(AF043636) circumsporozoite protein [Plasmodium chabaudi]	0.0001
15883	M11283	Aplysia californica FMRFamide mRNA, partial cds, clone FMRF-2.	0.007	3874685	(Z78539) Similarity to S.pombe hypothetical protein C4G8.04 (SW:YAD4_SC HPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come...	9e-013
15884	J03998	P.falciparum glutamic acid-rich protein gnen, complete cds.	0.003	<NONE>	<NONE>	<NONE>
15885	Z23143	M.musculus ALK-6 mRNA, complete CDS	0.002	2393890	(AF006064) protein kinase homolog [Fowlpox virus]	1e-011
15886	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	0.001	2136964	cysteine-rich hair keratin associated protein - rabbit >gi 510541 emb CAA56339 (X80035) cysteine rich hair keratin associated protein	1.9

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15887	AB012105	Brassica rapa mRNA for SLG45, complete cds	0.0008	3687246	(AC005169) putative suppressor protein [Arabidopsis thaliana]	5.5
15888	L41608	Methylobacterium extorquens (clone pDN9, HINDIIIAB) mxaS gene 3' end, mxaA, mxaC, mxaK, mxaL and mxaD genes, complete cds.	0.0008	3024235	NERVOUS-SYSTEM SPECIFIC OCTAMER-BINDING TRANSCRIPTION FACTOR N-OCT 3 PROTEIN)	5.1
15889	AB007914	Homo sapiens mRNA for KIAA0445 protein, complete cds	0.0008	2136964	cysteine-rich hair keratin associated protein - rabbit >gi 510541 emb CAA56339 (X80035) cysteine rich hair keratin associated protein	2.5
15890	AC002293	Genomic sequence from Human 9q34, complete sequence [Homo sapiens]	0.0008	2789557	(AF034316) MHC class I antigen [Triakis scyllium] scyllium]	0.0002
15891	L16013	Rattus norvegicus Q-like gene sequence	9e-005	<NONE>	<NONE>	<NONE>
15892	AF148512.1	Homo sapiens hexokinase II gene, promoter region	9e-005	<NONE>	<NONE>	<NONE>
15893	U94776	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	9e-005	4759138	solute carrier family 7 transporter 3 [Homo sapiens]	5.4

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15894	X56030	H.sapiens IAPP gene for amyloid polypeptide, exon 1	1e-005	<NONE>	<NONE>	<NONE>
15895	U36515	Human CT microsatellite, clone GM5927-CT-2-3, from the tandemly repeated genes encoding U2 small nuclear RNA (RNU2 locus)	4e-007	2435616	(AF026215) No definition line found [Caenorhabditis elegans]	0.85
15896	AB011119	Homo sapiens mRNA for KIAA0547 protein, complete cds	4e-007	4758508	airway trypsin-like protease [Homo sapiens]	3e-031
15897	NM_000521.1	Homo sapiens hexosaminidase B (beta polypeptide) (HEXB) mRNA	5e-008	2119379	slow muscle troponin T - chicken T [Gallus gallus]	2.8
15898	X13895	Human serum amyloid A (GSAA1) gene, complete cds	4e-008	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.7
15899	AB009288.1	Homo sapiens mRNA for N-copine, complete cds	4e-008	4520342	(AB008893) N-copine [Mus musculus]	3e-006
15900	AB011119	Homo sapiens mRNA for KIAA0547 protein, complete cds	4e-008	4758508	airway trypsin-like protease [Homo sapiens]	1e-028
15901	X13895	Human serum amyloid A (GSAA1) gene, complete cds	5e-009	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.8

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15902	X13895	Human serum amyloid A (GSAA1) gene, complete cds	2e-009	699405	(U18682) novel antigen receptor [Ginglymostoma cirratum]	7.2
15903	U64997	Bos taurus ribonuclease K6 gene, partial cds	2e-009	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi 2745760 (AF037086) ribonuclease k6 precursor	3e-018
15904	J02635	Rat liver alpha-2-macroglobulin mRNA, complete cds.	2e-009	112913	ALPHA-2-MACROGLOBULIN PRECURSOR precursor - rat >gi 202592 (J02635) prealpha-2-macroglobulin [Rattus norvegicus]	4e-019
15905	Z78141	M.musculus partial cochlear mRNA (clone 29C9)	5e-010	3219569	(AL023893) /prediction=(method;;	4e-009
15906	AF060917	Gambusia affinis microsatellite Gafu6	2e-010	3874618	(Z48241) similar to coiled coil domains; cDNA EST yk302g12.5 comes from this gene; cDNA EST yk365d10.5 comes from this gene; cDNA EST yk461c1.5 comes from this gene [Caenorhabditis elegans] coil domains; cDNA EST yk302g12.5 comes from this gene; cDNA EST	0.096

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15907	U68138	Human PSD-95 mRNA, partial cds	2e-010	4521241	(AB024927) CsENDO-3 [Ciona savignyi]	2e-022
15908	U88827	Aotus trivirgatus ribonuclease precursor gene, complete cds	6e-011	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) >gi 2745760 (AF037086) ribonuclease k6 precursor	1e-016
15909	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	2e-012	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	3e-016
15910	NM_001365.1	Homo sapiens discs, large (Drosophila) homolog 4 (DLG4) mRNA >:: gb U83192 HS U83192 Homo sapiens post-synaptic density protein 95 (PSD95) mRNA, complete cds	2e-012	4521241	(AB024927) CsENDO-3 [Ciona savignyi]	5e-020
15911	U28049	Human TBX2 (TBX2) mRNA, complete cds.	7e-013	2501115	TBX2 PROTEIN (T-BOX PROTEIN 2)	2e-011
15912	M23404	Chicken erythrocyte anion transport protein (band3) mRNA, complete cds.	2e-013	726403	(U23175) similar to anion exchange protein [Caenorhabditis elegans]	1e-025
15913	AF005963	Homo sapiens XY homologous region, partial sequence	1e-014	104270	Ig heavy chain - clawed frog	1.9

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15914	M29863	Human farnesyl pyrophosphate synthetase mRNA	9e-015	182405	(M29863) farnesyl pyrophosphate synthetase [Homo sapiens]	0.005
15915	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	3e-015	<NONE>	<NONE>	<NONE>
15916	Z80150	H.sapiens CACNL1A4 gene, exons 41 and 42 > :: emb A70716.1 A70716 Sequence 37 from Patent WO9813490	3e-015	3387914	(AF070550) cotel [Homo sapiens]	3.5
15917	U28049	Human TBX2 (TXB2) mRNA, complete cds.	4e-016	2501116	TBX2 PROTEIN (T-BX BOX PROTEIN 2) tbx gene [Mus musculus]	6e-009
15918	U31629	Mus musculus C2C12 unknown mRNA, partial cds.	1e-017	3024998	HYPOTHETICAL HEART PROTEIN	3e-017
15919	J05262	Human farnesyl pyrophosphate synthetase mRNA, complete cds.	1e-018	182405	(M29863) farnesyl pyrophosphate synthetase [Homo sapiens]	0.0001
15920	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	5e-019	<NONE>	<NONE>	<NONE>
15921	D28126	Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	5e-019	3219984	HYPOTHETICAL PROTEIN MJ1597.1 region MJ1597.1 [Methanococcus jannaschii]	5.7

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15922	NM_004587.1	Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1) mRNA > :: gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds	2e-019	4759056	ribosome binding protein 1 (dog 180kD homolog) > gi 3299885 (AF006751) ES/130 [Homo sapiens]	0.004
15923	U89915	Mus musculus junctional adhesion molecule (Jam) mRNA, complete cds	5e-020	3462455	(U89915) junctional adhesion molecule [Mus musculus]	2e-005
15924	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	5e-020	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	9e-025
15925	NM_004587.1	Homo sapiens ribosome binding protein 1 (dog 180kD homolog) (RRBP1) mRNA > :: gb AF006751 AF006751 Homo sapiens ES/130 mRNA, complete cds	2e-020	4759056	ribosome binding protein 1 (dog 180kD homolog) > gi 3299885 (AF006751) ES/130 [Homo sapiens]	0.0008
15926	AF051098	Mus musculus seven transmembrane domain orphan receptor mRNA, complete cds	2e-021	3858883	(U67056) myosin I heavy chain kinase [Acanthamoeba castellanii] > gi 4206769 (AF104910) myosin I heavy chain kinase [Acanthamoeba castellanii]	0.002

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15927	AF051098	Mus musculus seven transmembrane domain orphan receptor mRNA, complete cds	2e-021	3858883	(U67056) myosin I heavy chain kinase [Acanthamoeba castellanii] > gi 4206769 (AF104910) myosin I heavy chain kinase [Acanthamoeba castellanii]	0.001
15928	M13519	Human N-acetyl-beta-glucosaminidase (HEXB) mRNA, 3' end.	2e-021	4504373	hexosaminidase B (beta polypeptide) > gi 123081 sp P07686 HEXB_HUMAN BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR beta-N-acetylhexosaminidase (EC 3.2.1.52) beta chain - human > gi 386770 (M23294) beta-hexosaminidase beta-subunit [Homo sapiens]	2e-007
15929	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	2e-022	< NONE >	< NONE >	< NONE >

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15930	AF147311.1	Homo sapiens full length insert cDNA clone YA82F10	2e-022	3875904	(Z70207) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65905 comes from this gene; cDNA EST EMBL:D65858 comes from this gene; cDNA EST EMBL:D69306 comes from this gene; cDNA EST EMBL:D65755 comes from this gen...	0.07
15931	AF037088	Gorilla gorilla ribonuclease k6 precursor, gene, complete cds	9e-024	3914791	RIBONUCLEASE K6 PRECURSOR (RNASE K6) > gi 2745752 (AF037082) ribonuclease k6 precursor	3e-019
15932	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	8e-024	<NONE>	<NONE>	<NONE>
15933	AF037088	Gorilla gorilla ribonuclease k6 precursor, gene, complete cds	9e-025	3914810	RIBONUCLEASE K6 PRECURSOR (RNASE K6) > gi 2745760 (AF037086) ribonuclease k6 precursor	4e-018

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15934	AF147311.1	Homo sapiens full length insert cDNA clone YA82F10	1e-026	131413	PULMONARY SURFACTANT-ASSOCIATED PROTEIN A PRECURSOR (SP-A) (PSP-A) (PSAP) precursor - rabbit > gi 165706 (J03542) apoprotein of surfactant [Oryctolagus cuniculus]	0.059
15935	Z46786	D.melanogaster mRNA for acetyl-CoA synthetase	1e-027	1079042	acetyl-CoA synthetase - fruit fly	4e-025
15936	NM_004039.1	Homo sapiens annexin II (lipocortin II) for lipocortin II, complete cds	4e-028	450448	(M33322) calpactin I heavy chain [Mus musculus]	0.1
15937	X53064	Homo sapiens SPRR2A gene encoding small proline rich protein	1e-028	134846	SMALL PROLINE-RICH PROTEIN II rich protein [Homo sapiens]	0.005
15938	M29863	Human farnesyl pyrophosphate synthetase mRNA	1e-028	4503685	farnesyl diphosphate synthase dimethylallyltransferase, geranyltransferase) bp313 to bp1374 is almost identical to human farnesyl pyrophosphate synthetase mRNA. [Homo sapiens]	2e-008

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15939	Z18950	H.sapiens genes for S100E calcium binding protein, CAPL, and S100D calcium binding protein EF-Hand patent US 5789248	5e-029	2493898	DOPAMINE-BETA-MONOOXYGENASE PRECURSOR (DOPAMINE BETA-HYDROXYLASE) (DBH) 1.14.17.1) precursor - mouse >gi 260873 bb s 119249 621 aa] [Mus sp.]	1.4
15940	M19481	Human follistatin gene, exon 6.	5e-030	<NONE>	<NONE>	<NONE>
15941	AF007155	Homo sapiens clone 23763 unknown mRNA, partial cds	2e-032	4502641	chemokine (C-C) receptor 7 TYPE 7 PRECURSOR (C-C CKR-7) (CC-CKR-7) (CCR-7) (MIP-3 BETA RECEPTOR) (EBV-INDUCED G PROTEIN-COUPLED RECEPTOR 1) (EBI1) (BLR2) >gi 1082381 p ir B55735 lymphocyte-specific G-protein-coupled receptor EBI1 - human >gi 468316 (L3158	1.6
15942	M99624	Human epidermal growth factor receptor-related gene, 5' end.	8e-034	294845	(L13655) membrane protein [Saccharum hybrid cultivar H65-7052]	9e-014

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15943	U49082	Human transporter protein (g17) mRNA, complete cds	8e-035	1840045	(U49082) transporter protein [Homo sapiens]	1e-014
15944	D50369	Homo sapiens mRNA for low molecular mass ubiquinone-binding protein, complete cds	9e-036	3024781	UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX UBIQUINONE-BINDING PROTEIN QP-C PROTEIN) (COMPLEX III SUBUNIT VII) ubiquinone-binding protein [Homo sapiens]	0.0002
15945	AF086313	Homo sapiens full length insert cDNA clone ZD52B10	9e-036	2832777	(AL021086) /prediction=(method:; comes from the 5' UTR [Drosophila melanogaster]	1e-039
15946	NM_004074.1	Homo sapiens cytochrome c oxidase subunit VIII (COX8), nuclear gene encoding mitochondrial protein, mRNA > :: gb J04823 HU MCOX8A Human cytochrome c oxidase subunit VIII (COX8) mRNA, complete cds.	1e-038	2499854	PROBABLE PEPTIDASE Y4SO > gi 2182630	2

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15947	AB024436.1	Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds	2e-041	3132900	(AF038662) beta-1,4-galactosyltransferase [Homo sapiens] beta-1,4-galactosyltransferase IV [Homo sapiens]	4e-016
15948	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	2e-043	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	3e-062
15949	Z69650.1	Human DNA sequence from cosmid L69F7B, Huntington's Disease Region, chromosome 4p16.3 contains Huntington Disease (HD) gene	2e-044	1872200	(U22376) alternatively spliced product using exon 13A	1e-008
15950	NM_003938.1	Homo sapiens adaptin, delta (ADTD) mRNA > :: gb U91930 HS U91930 Homo sapiens AP-3 complex delta subunit mRNA, complete cds	2e-044	3478639	(AC005545) delta-adaptin, partial CDS [Homo sapiens]	3e-016
15951	AF026029	Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds	8e-045	1916930	(U88570) CREB-binding protein homolog [Drosophila melanogaster]	7.6

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15952	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	1e-045	73404	E2 protein - human papillomavirus type 5	0.11
15953	U90918	Human clone 23654 mRNA sequence	1e-048	3877568	(Z70208) similar to collagen	0.042
15954	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	1e-049	73404	E2 protein - human papillomavirus type 5	0.11
15955	AL049258.1	Homo sapiens mRNA; cDNA DKFZp564E173 (from clone DKFZp564E173)	1e-050	<NONE>	<NONE>	<NONE>
15956	AF022367	Homo sapiens beta-1,4-galactosyltransferase mRNA, complete cds	5e-051	3132900	(AF038662) beta-1,4-galactosyltransferase [Homo sapiens] beta-1,4-galactosyltransferase IV [Homo sapiens]	6e-019
15957	AF057734	Homo sapiens 17-beta-hydroxysteroid dehydrogenase IV (HSD17B4) gene, exon 16	7e-053	2842416	(AL008730) dJ487J7.1.1 (putative protein dJ487J7.1 isoform 1) [Homo sapiens]	6e-055
15958	AF097709	Homo sapiens serine protease (PRSS11) mRNA, partial cds	8e-055	4506141	protease, serine, 11 (IGF binding) > gi 1513059 d bj BAA13322 (D87258) serin protease with IGF-binding motif [Homo sapiens] protease, PRSS11 [Homo sapiens]	2e-017

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15959	U31629	Mus musculus C2C12 unknown mRNA, partial cds.	9e-057	3025215	HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME III > gi 2146877 p ir S72572 probable ABC1 protein homolog - Caenorhabditis elegans protein (Swiss-Prot Acc: P27697) [Caenorhabditis elegans]	5e-033
15960	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	8e-057	73404	E2 protein - human papillomavirus type 5	1.7
15961	AF025439	Homo sapiens Opa-interacting protein OIP3 mRNA, partial cds	4e-059	<NONE>	<NONE>	<NONE>
15962	M99624	Human epidermal growth factor receptor-related gene, 5' end.	1e-060	123364	SEGMENTATION PROTEIN EVEN-SKIPPED fly (Drosophila sp.) > gi 157387 (M14767) even-skipped gene [Drosophila melanogaster]	5.3
15963	AF045573	Mus musculus FLI-LRR associated protein-1 mRNA, complete cds	5e-061	3025718	(AF045573) FLI-LRR associated protein-1 [Mus musculus]	7e-029
15964	AB006622	Homo sapiens mRNA for KIAA0284 gene, partial cds	2e-062	2119133	ribosomal protein S17 - cat (fragment) musculus]	2e-015

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15965	M30702	Human amphiregulin (AR) gene, exon 5, clones lambda-ARH(6,12).	2e-063	4502199	amphiregulin (schwannoma-derived growth factor) > gi 113754 sp P15514 AMP R_HUMAN AMPHIREGULIN PRECURSOR (AR) (COLORECTUM CELL-DERIVED GROWTH FACTOR) (CRDGF) > gi 107391 pir A34702 amphiregulin precursor - human > gi 178890 (M30703) amphiregulin [Homo sapien	0.0002
15966	L38847	Mus musculus hepatoma transmembrane kinase ligand Sequence 1 from patent US 5624899	6e-064	3861228	(AJ235272) unknown [Rickettsia prowazekii]	2.9
15967	L38847	Mus musculus hepatoma transmembrane kinase ligand Sequence 1 from patent US 5624899	6e-064	3861228	(AJ235272) unknown [Rickettsia prowazekii]	2.9
15968	Z78141	M.musculus partial cochlear mRNA (clone 29C9)	8e-066	1490324	(Z78141) unknown [Mus musculus]	8e-019
15969	X12650	Mus musculus gene for beta-tropomyosin	2e-072	833602	(X54277) cardiac tropomyosin [Coturnix coturnix]	7e-022

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15970	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	2e-084	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	5e-019
15971	M13364	Rabbit calcium-dependent protease, small subunit mRNA, complete cds.	2e-084	115611	CALCIUM-DEPENDENT PROTEASE, SMALL NEUTRAL PROTEINASE) (CANP) > gi 108563 pir A34466 calpain (EC 3.4.22.17) II light chain - bovine 3.4.22.17) [Bos taurus]	1e-058
15972	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	3e-088	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	9e-028
15973	M87635	Mouse beta-tropomyosin 2 mRNA, complete cds.	5e-092	1216293	(L35239) cardiac tropomyosin [Xenopus laevis]	2e-035
15974	X85992	M. musculus mRNA for semaphorin C	8e-097	2137756	semaphorin C - mouse (fragment) musculus]	2e-048
15975	M24103	Bovine ADP/ATP translocase T2 mRNA, complete cds.	e-103	113463	ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3) > gi 86757 pir S03894 ADP,ATP carrier protein T2 - human	2e-035

Table 121

	Nearest Neighbor (BlastN vs. Genbank)			Nearest Neighbor (BlastX vs. Non-Redundant Proteins)		
15976	U48852	Cricetulus griseus HT protein mRNA, complete cds.	e-107	1216486	(U48852) HT protein [Cricetulus griseus]	3e-057
15977	X76168	R.norvegicus mRNA for connexin 30.3	e-112	544118	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) >gi 481577 pir S38891 connexin 30.3 - rat >gi 431204 emb CAA53762 (X76168) connexin 30.3	1e-063
15978	X76168	R.norvegicus mRNA for connexin 30.3	e-115	461864	GAP JUNCTION BETA-5 PROTEIN junction protein Cx30.3 - mouse >gi 192647(M91443) connexin 30.3 [Mus musculus]	7e-064
15979	AJ009634.1	Mus musculus fjl1 gene	e-137	4138203	(AJ009634) Fjl1 [Mus musculus]	5e-065
15980	X76168	R.norvegicus mRNA for connexin 30.3	e-130	544118	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) >gi 481577 pir S38891 connexin 30.3 - rat >gi 431204 emb CAA53762 (X76168) connexin 30.3	2e-074

Example 79: Differential Expression of Polynucleotides of the Invention: Description of Libraries and

Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including primary cells, cell lines and patient tissue samples. Table 122 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Table 122. Description of cDNA Libraries

Library (Lib#)	Description	Number of Clones in Library
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMVEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMVEC) – bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMVEC) – VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR	36216

Library (Lib#)	Description	Number of Clones in Library
	(OligodT) cDNA library)	
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23-	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349

The KM12L4 cell line is derived from the KM12C cell line (Morikawa, et al., *Cancer Research* (1988) 48:6863). The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B₂ surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KML4-A is a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*; Yeatman et al. *Clin. Exp. Metastasis* (1996) 14:246). The MDA-MB-231 cell line (Brinkley et al. *Cancer Res.* (1980) 40:3118-3129) was originally isolated from pleural effusions (Cailleau, *J. Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma.

The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see,

e.g., Chandrasekaran *et al.*, *Cancer Res.* (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar *et al.*, *J Med Chem* (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson *et al.*, *Br J Cancer* (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang *et al.*, *Nucleic Acids Res* (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki *et al.*, *Int J Cancer* (1987) 40:46 (UCP-3); Varki *et al.*, *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki *et al.*, *Anticancer Res.* (1990) 10:637; (MV-522); Kelner *et al.*, *Anticancer Res* (1995) 15:867 (MV-522); and Zhang *et al.*, *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cells were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz cells were derived from normal prostate epithelium. The WOca cells are Gleason Grade 4 cell line.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related

cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

Using this approach, a number of polynucleotide sequences were identified as being differentially expressed between, for example, cells derived from high metastatic potential cancer tissue and low metastatic cancer cells, and between cells derived from metastatic cancer tissue and normal tissue. Evaluation of the levels of expression of the genes corresponding to these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes corresponding to differentially expressed sequences described herein can be therapeutic targets due to their involvement in regulation (*e.g.*, inhibition or

promotion) of development of, for example, the metastatic phenotype. For example, sequences that correspond to genes that are increased in expression in high metastatic potential cells relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

Detection of the relative expression levels of differentially expressed polynucleotides described herein can provide valuable information to guide the clinician in the choice of therapy. For example, a patient sample exhibiting an expression level of one or more of these polynucleotides that corresponds to a gene that is increased in expression in metastatic or high metastatic potential cells may warrant more aggressive treatment for the patient. In contrast, detection of expression levels of a polynucleotide sequence that corresponds to expression levels associated with that of low metastatic potential cells may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of the polynucleotides described herein can thus be used as, for example, diagnostic markers, prognostic markers, for risk assessment, patient treatment and the like. These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers.

The differential expression data for polynucleotides of the invention that have been identified as being differentially expressed across various combinations of the libraries described above is summarized in Table 123 (inserted prior to the claims). Table 123 provides: 1) the Sequence Identification Number ("SEQ ID") assigned to the polynucleotide; 2) the cluster ("CLUST") to which the polynucleotide has been assigned as described above; 3) the library comparisons that resulted in identification of the polynucleotide as being differentially expressed ("PairAB-text"), with shorthand names of the compared libraries provided in parentheses following the library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("B"); 6) the "RATIO PLUS" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "RATIO MINUS" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
15670	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15674	728115					
		_15,16 (Normal Colon vs. Colon Tumor)	0	7		6.62
		_16,17 (Colon Tumor vs. Colon Metastasis)	7	0	7.11	
15675	372700					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	3	50		11.93
		_19,20 (Colon Tumor vs. Colon Tumor Metastasis)	8	0	5.98	
15678	729832					
		_15,16 (Normal Colon vs. Colon Tumor)	0	11		10.41
		_16,17 (Colon Tumor vs. Colon Metastasis)	11	0	11.17	
15679	505514					
		_23,24 (Normal Lung vs. Lung Tumor)	26	10	2.63	
15683	549934					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	0	7.87	
		_16,17 (Colon Tumor vs. Colon Metastasis)	3	20		6.56
		_15,16 (Normal Colon vs. Colon Tumor)	11	3	3.88	
15691	450399					
		_15,16 (Normal Colon vs. Colon Tumor)	28	68		2.3
		_15,17 (Normal Colon vs. Colon Metastasis)	28	117		3.89
15692	450982					
		_16,17 (Colon Tumor vs. Colon Metastasis)	14	32		2.25
15694	379302					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	1	7.87	

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
15709	817503					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	4	4.43	
15714	830085					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	9		9.15
15718	830931					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
15721	819046					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	13		6.61
15724	728115					
		_15,16 (Normal Colon vs. Colon Tumor)	0	7		6.62
		_16,17 (Colon Tumor vs. Colon Metastasis)	7	0	7.11	
15731	553242					
		_16,17 (Colon Tumor vs. Colon Metastasis)	0	6		5.91
15737	820061					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	20		20.33
15744	220584					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	1	12		8.59
15746	549934					
		_16,17 (Colon Tumor vs. Colon Metastasis)	3	20		6.56
		_15,16 (Normal Colon vs. Colon Tumor)	11	3	3.88	
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	0	7.87	
15752	819460					
		_21,22 (Normal Prostate vs.	18	1	17.7	

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		Cancerous Prostate)				
15761	551785					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
15762	17092					
		_03,04 (Breast, High Metastatic Potential vs. Breast, Non-Metastatic)	0	25		25.62
15765	745559					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	9		9.15
15767	379879					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	9		9.15
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	13		9.3
15773	268290					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	33	69		2.13
15774	818043					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15780	450247					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	23	8	2.83	
15781	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15782	587779					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15784	615617					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONE S in B	RATIO PLUS	RATIO MINUS
15787	818682					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	2	5.41	
15789	484413					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15790	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15793	818682					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	2	5.41	
15797	819273					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15813	820061					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	1	20		20.33
15819	375958					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	11		5.59
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	9		6.44
15821	831049					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	11		11.18
15823	553200					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
15824	139677					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15825	139677					

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15829	375958					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	9		6.44
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	11		5.59
15834	831812					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
15842	193373					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15843	400619					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	6	0	8.38	
15844	831149					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
15846	817503					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	4	4.43	
15853	648679					
		_23,24 (Normal Lung vs. Lung Tumor)	11	1	11.11	
		_16,17 (Colon Tumor vs. Colon Metastasis)	79	0	80.23	
		_15,17 (Normal Colon vs. Colon Metastasis)	7	0	7.51	
		_15,16 (Normal Colon vs. Colon Tumor)	7	79		10.68
15856	373928					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15861	373928					

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONES in B	RATIO PLUS	RATIO MINUS
		_21,22 (Normal Prostate vs. Cancerous Prostate)	7	0	6.88	
15864	372700					
		_19,20 (Colon Tumor vs. Colon Tumor Metastasis)	8	0	5.98	
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	3	50		11.93
15870	379105					
		_15,16 (Normal Colon vs. Colon Tumor)	0	8		7.57
15871	831188					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	8		8.13
15875	831812					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	7		7.12
15879	831026					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	10		10.17
15881	380207					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	0	8		5.72
15882	819460					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	18	1	17.7	
15890	819201					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15891	374826					
		_15,17 (Normal Colon vs. Colon Metastasis)	5	20		3.73
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low	38	132		2.49

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONE S in B	RATIO PLUS	RATIO MINUS
		Metastatic Potential)				
		_15,16 (Normal Colon vs. Colon Tumor)	5	18		3.41
15897	553242					
		_16,17 (Colon Tumor vs. Colon Metastasis)	0	6		5.91
15912	220584					
		_08,09 (Lung, High Metastatic Potential vs. Lung, Low Metastatic Potential)	1	12		8.59
15914	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15919	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	
15922	831160					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	12		12.2
15925	831160					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	12		12.2
15928	373298					
		_15,17 (Normal Colon vs. Colon Metastasis)	126	42	3.22	
		_15,16 (Normal Colon vs. Colon Tumor)	126	59	2.26	
15936	450262					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	8		8.13
15937	484703					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	28	0	27.54	
15938	819498					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	6	0	5.9	

Table 123

SEQ ID	CLUST	PairAB-text	CLONES in A	CLONE S in B	RATIO PLUS	RATIO MINUS
15939	406043					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
15940	817500					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	18		9.15
15941	818180					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	2	10		5.08
15946	429009					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	8	1	7.87	
15950	383021					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	3	12		4.07
15955	831580					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	0	6		6.1
15977	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
15978	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
15980	763446					
		_21,22 (Normal Prostate vs. Cancerous Prostate)	11	1	10.82	
15981	10154					
		_3,4 (Breast,High Metastatic Potential vs. Breast, Low Metastatic)	3	317		108.1

Example 80: Differential Expression of a Polynucleotides Associated with Metastatic Potential in Breast Cancer

- 5 Differential expression was examined in breast cancer cells having either high metastatic potential or low metastatic potential. A single cluster, Cluster Identification No. 10154, was identified as displaying low expression in the high metastatic potential breast

cancer cells (Library 3), and significantly increased expression – approximately 100-fold higher -- in the low metastatic potential cells (Library 4). Specifically, three clones were identified that were expressed in Library 3, the high metastatic potential breast cancer library, while 317 clones were expressed in Library 4, the low metastatic potential breast cancer library. The two sequences assigned to this particular cluster, SEQ ID NO:15981 and SEQ ID NO:15982, both displayed this differential expression, suggesting that the two sequences are likely associated with a single transcript.

SEQ ID NO: 15981 and SEQ ID NO: 15982 were then used as query sequences to search for homologous sequences in GenBank as described above. SEQ ID NO: 15981 displayed identity to the GenBank entry H72034 (SEQ ID NO: 15983) and SEQ ID NO: 15982 displayed identity to GenBank entry AA707002 (SEQ ID NO: 15984). SEQ ID NO: 15981 displays striking identity to the 3' end of SEQ ID NO: 15983 (See Figures 1A and 1B), while SEQ ID NO: 15982 displays striking identity to the 5' end of SEQ ID NO: 15984 (See Figure 2). Clones of H72034 and AA707002 were ordered from the I.M.A.G.E. Consortium at the Lawrence Livermore National Laboratories (Livermore, California) for further studies.

Restriction Mapping of Clones H72034 and AA707002

The newly identified sequences were digested with a number of different restriction endonucleases to construct a restriction map of each of the clones. An appropriate amount of each clone, SEQ ID NO: 15983 or SEQ ID NO: 15984, was digested with various enzymes, and the restriction fragments identified as follows:

SEQ ID NO: 15983

Enzyme	#Cuts	Positions								
AluI	5	331	1029	1422	1595	1977				
BamHI	2	1836	2089							
BstEII	1	936								
BstXI	1	1033								
HaeIII	12	145	300	453	497	582	780			
		1102	1536	1561	1722	1981	2062			
HinfI	12	5	154	205	325	397	473	610	820	
			1295	1426	2066					
KpnI	1	1938								
MspI	6	78	739	1098	2038	2077	2093			
NcoI	2	2013	2058							
PstI	1	1501								
PvuII	2	331	1422							
Sau3AI	6	1270	1813	1819	1836	1894	2089			
SphI	1	1870								
XhoI	1	1413								

SEQ ID NO: 15984

Enzyme	#Cuts	Positions								
AluI	9	19	245	367	553	586	874	904	996	
BamHI	1	407								
BglI	1	1056								
BglII	1	475								
BstEI	1	1108								
HaeIII	10	153	348	485	867	518	628	780	867	
			1016	1312						
HindIII	2	243	872							
HinfI	1	1353								
KpnI	1	132								
MspI	2	1196	1261							
PstI	1	823								
PvuII	1	996								
Sau3AI	7	66	407	475	504	750	850	1024		

The restriction maps based on the identified sites can be used to determine the position of each clone relative to the genomic sequences, and to confirm the 5'-3' orientation of the clones.

Amplification and Purification of Transcript

A transcript in this region upregulated in low metastatic cancers which contain sequences from SEQ ID NOS: 15983-15986-318 is identified using a technique such as polymerase chain reaction (PCR) amplification. Based on the sequences identified and the

original sequences of the cluster, primers can be designed to isolate the full length cDNA from a library constructed from the breast cancer cell line with low metastatic potential.

A cDNA template for use in the amplification reaction is generated from total RNA isolated from the high metastatic breast cell line. RNA is reverse transcribed using oligo-dT primer to generate first strand cDNA. cDNA is synthesized by denaturing 3:1 of total RNA, 2 :1 oligo-dT primer at 20 :M, and 5 :1 DEPC water for 8 minutes at 65°C followed by reverse transcription at 52°C for 1 hour in a reaction containing the denatured RNA/primer plus 4:1 1 5X cDNA buffer (GibcoBRL), 1 :1 0.1 M dithiothreitol, 1 :1 40 U/1 RNaseOUT (GibcoBRL), 1 :1 DEPC water, 2 :1 10 mM dNTP (GibdoBRL), and 1 :1 15 U/1 Thermoscript reverse transcriptase (GibcoBRL). The reaction was terminated by a 5-min incubation at 85°C, and the RNA was removed by 1 :1 2 U/1 RNase H at 37°C for thirty minutes.

Based on the determined orientation of the clones, primers are designed to amplify a full-length clone corresponding to the differentially expressed transcript in this region. Forward primers that are used to amplify the full-length clone are taken from the 5' end of SEQ ID NO:15683 as follows:

F1 5'- TGGGATATAGTCTCGTGGTGCG -3' (SEQ ID NO:15985)

F2 5'- TGATTCGATGTCATCAGTCCCG-3' (SEQ ID NO:15986)

Primer F1 is taken from residues 51-62 of SEQ ID NO: 15983, and primer F2 is taken from residues 212-233 Of SEQ ID NO:15683. Both forward primers are near the 5' end of this sequence.

Reverse Primers are designed using sequences complementary to the 3' end of clone 10154-3 as follows:

R1 5'- TGTGTCACAGCCAGACATGAGC (SEQ ID NO: 15987)

R2 5' – TGCAAACATACACAGGGACCG (SEQ ID NO: 15988)

Primer R1 is based on residues 573-552 of SEQ ID NO:15684, and R2 is based on residues 399-379 of SEQ ID NO:15684.

PCR is performed using a 5:1 aliquot of the first strand cDNA synthesis reaction, and a primer pair, e.g., F1 and R1, F1 and R2, F2 and R1, or F2 and R2. An open reading

frame is amplified using 2 :l of the reverse transcription product as template in a PCR reaction containing 5 :l of 10x PCR buffer (GibcoBRL), 1 :l 50 mM Mg₂SO₄, 1 :l 10 mM dNTP, 1 :l F1 or F2 primer, 1 µl R1 primer, 2.5 U High Fidelity Platinum Taq DNA polymerase (GibcoBRL), and water to 50 :l. The molecule is amplified using 30 rounds of
5 amplification in a thermal cycler at the following temperatures: 1 minute at 95°C; 1 minute at 55°C and 2 minutes at 72°C. The 30 cycles was followed by a 10 minute extension at 72°C.

Following amplification of the sequences, the PCR products are loaded on a 1% TEA gel and subjected to gel purification. One or more bands can be isolated from the gel
10 and the DNA was purified using a QIAquick® Gel Extraction Kit (Qiagen, Valencia, CA). The purified fragment was cloned into a bacterial vector and transformed into the bacterial strain DH5V. Following cloning of the purified fragment(s), the DNA can be isolated and sequenced to confirm that a band corresponds to a transcript from this genetic region.

The reactions are carried out with two different 5' and 3' primers to increase the
15 likelihood that the reaction will yield an amplification product. Other primers may also be designed from the predicted 5' and/or 3' end of the sequence, as will be apparent to one skilled in the art upon reading this disclosure, and thus other primers may be designed from the general region of SEQ ID NOS:317 and 318 that may yield better results than the disclosed primers.

20 In order to obtain additional sequences 5' to the end of a partial cDNA, 5' rapid amplification of cDNA ends (RACE) can be performed to ensure that the entire transcript has been identified. See *PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc. Following isolation of a cDNA using the F1-R1 or F2-R1 primer pairs, additional primers can be designed to perform RACE. The primers can be designed
25 from the sequence of 10154-1 as follows:

5'-TTTAGCAGCACTAATGACTGTGGC-3' (SEQ ID NO:15989)
5'-CGCCGTGAATTACTGTGGATGG-3' (SEQ ID NO:15990)

30 The two RACE primers are designed based residues 286-263 and 396-375 of SEQ ID NO:15983, respectively.

These sequences can be used to obtain any transcript sequences 5' to the amplification products obtained using the PCR protocol described above.

Northern Analysis

Other techniques can be used for confirming differential expression of the full-length transcript. For example, a Northern Blot can be used to verify differential expression of SEQ ID NOS:15983 and 15984 in a breast cancer cells with low metastatic potential compared to breast cancer cells with high metastatic potential. Northern analysis can be accomplished by methods well-known in the art. Briefly, RNA is individually isolated from breast cancer cells having high metastatic potential and breast cancer cells having low metastatic potential, *e.g.*, a product such as RNeasy Mini Kits (Qiagen, CA) or NucleoSpin® RNA II Kit (Clontech, Palo Alto, CA). The isolated RNA samples are For Northern analysis, RNA isolated from the cells was electrophoresed on a denaturing formaldehyde agarose gel and transferred onto a membrane such as a supported nitrocellulose membrane (Schleicher & Schuell).

Rapid-Hyb buffer (Amersham Life Science, Little Chalfont, England) with 5 mg/ml denatured single stranded sperm DNA is pre-warmed to 65°C and the RNA blots are pre-hybridized in the buffer with shaking at 65°C for 30 minutes. Gene-specific DNA probes (50 ng per reaction) labeled with [α -³²P]dCTP (3000Ci/mmol, Amersham Pharmacia Biotech Inc., Piscataway, NJ) (Prime-It RmT Kit, Stratagene, La Jolla, CA) and purified with ProbeQuant™ G-50 Micro Columns (Amersham Pharmacia Biotech Inc.) are added and hybridized to the blots with shaking at 65°C for overnight. The blots are washed in 2x SSC, 0.1%(w/v) SDS at room temperature for 20 minutes, twice in 1x SSC, 0.1%(w/v) SDS at 65°C for 15 minutes, then exposed to Hyperfilms (Amersham Life Science).

Example 81: Identification of Differentially Expressed Genes by Array Analysis with Patient Tissue Samples

Differentially expressed genes corresponding to the polynucleotides described herein were also identified by microarray hybridization analysis using materials obtained from patient tissue samples. The biological materials used in these experiments are described below.

Source of patient tissue samples

Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, *e.g.*, Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet*

14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001). Table 127 (inserted following the last page of the Examples) provides information about each patient from which the samples were isolated, including: the Patient ID and Path ReportID, numbers assigned to the patient and the pathology reports for identification purposes; the anatomical location of the tumor (AnatomicalLoc); The Primary Tumor Size; the Primary Tumor Grade; the Histopathologic Grade; a description of local sites to which the tumor had invaded (Local Invasion); the presence of lymph node metastases (Lymph Node Metastasis); incidence of lymph node metastases (provided as number of lymph nodes positive for metastasis over the number of lymph nodes examined) (Incidence Lymphnode Metastasis); the Regional Lymphnode Grade; the identification or detection of metastases to sites distant to the tumor and their location (Distant Met & Loc); a description of the distant metastases (Description Distant Met); the grade of distant metastasis (Distant Met Grade); and general comments about the patient or the tumor (Comments). Adenoma was not described in any of the patients. ; adenoma dysplasia (described as hyperplasia by the pathologist) was described in Patient ID No. 695. Extranodal extensions were described in two patients, Patient ID Nos. 784 and 791. Lymphovascular invasion was described in seven patients, Patient ID Nos. 128, 278, 517, 534, 784, 786, and 791.. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Source of polynucleotides on arrays

Polynucleotides on arrays

Polynucleotides spotted on the arrays were generated by PCR amplification of clones derived from cDNA libraries. The clones used for amplification were either the clones from which the sequences described herein were derived, or are clones having inserts with significant polynucleotide sequence overlap with the sequences described herein (SEQ ID NO:15667-15982) as determined by BLAST2 homology searching.

Microarray Design

Each array used in the examples below had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the

manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides.

The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

Microarray analysis

cDNA probes were prepared from total RNA isolated from the patient cells described in above (Table 127). Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling. Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red).

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After

hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level of fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. For initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations

are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

Table 128 below summarize the results of the differential expression analysis. Each table provides: the SEQ ID NO of the polynucleotide corresponding to the polynucleotide on the spot on the array; the Spot ID (an identifier assigned to the spot so as to distinguish it from spots on the same and different arrays), the number of patients for whom there was information obtained from the array (Num Ratios), and the percentage of patients in which expression was detected at greater than or equal to a two-fold increase ($\geq 2x$), greater than or equal to a five-fold increase ($\geq 5x$), or less than or equal to a 1/2 -fold decrease ($\leq \text{halfx}$) relative to matched normal control tissue.

In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at least one sample and the ratio value is greater than at least about 1.2 fold, preferably greater than at least about 1.5 fold, more preferably greater than at least about 2 fold, where the ratio value is calculated using the method described above.

A differential expression ratio of 1 indicates that the expression level of the gene in the tumor cell was not statistically different from expression of that gene in normal colon cells of the same patient. A differential expression ratio significantly greater than 1 in cancerous colon cells relative to normal colon cells indicates that the gene is increased in expression in cancerous cells relative to normal cells, indicating that the gene plays a role in the development of the cancerous phenotype, and may be involved in promoting metastasis of the cell. Detection of gene products from such genes can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target.

Likewise, a differential expression ratio significantly less than 1 in cancerous colon cells relative to normal colon cells indicates that, for example, the gene is involved in suppression of the cancerous phenotype. Increasing activity of the gene product encoded by such a gene, or replacing such activity, can provide the basis for chemotherapy. Such gene can also serve as markers of cancerous cells, e.g., the absence or decreased presence of the gene product in a colon cell relative to a normal colon cell indicates that the cell may be cancerous.

Table 128.

SEQ ID NO:	SpotID	Num Ratios	$\geq 2x$	$\geq 5x$	$\leq \text{halfx}$
------------	--------	------------	-----------	-----------	---------------------

15674	579	33	87.88	39.39	3.03
15678	22300	33	33.33	18.18	6.06
15692	21886	33	33.33	0.00	3.03
15730	9487	33	33.33	12.12	3.03
15914	28179	28	32.14	0.00	0.00
15919	28179	28	32.14	0.00	0.00
15938	28179	28	32.14	0.00	0.00
15958	9111	33	33.33	18.18	3.03
15961	19980	33	33.33	6.06	0.00
15975	23993	33	42.42	3.03	3.03

Deposit Information. The following materials were deposited with the American Type Culture Collection (CMCC = Chiron Master Culture Collection).

5 **Table 124.** Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 6 below provides the ATCC Accession Nos. of the ES deposits, all of which were deposited on or before May 13, 1999. The names of the clones contained within each of these
10 deposits are provided in the Table 126 (inserted before the claims).

Table 125: Pools of Clones and Libraries Deposited with ATCC on or before March 28, 2000

Cell Line	CMCC	ATCC
ES75	5140	PTA-1102
ES76	5141	PTA-1103
ES77	5142	PTA-1104
ES78	5143	PTA-1105
ES79	5144	PTA-1106
ES80	5145	PTA-1107
ES81	5146	PTA-1108
ES82	5147	PTA-1109
ES83	5148	PTA-1110
ES84	5149	PTA-1111

Table 126

Library No.

Clones

es75

M00063947D:D01

es79 M000640

03B:C10

	M00063158A:A01		M000643
			02A:D10
	M00063517A:A04		M000643
			09C:H09
	M00063520D:E11		M000643
			10D:F03
	M00063638C:G12		M000643
			22C:A10
	M00063642B:A08		M000643
			59B:H12
	M00063686B:E07		M000643
			90A:C05
	M00063689D:E12		M000644
			04A:B05
	M00063781B:B10		M000644
			04C:G05
	M00063826A:D03		M000644
			04D:A06
es76	M00063838B:G08	es80	M000644
			29D:B07
	M00063838B:G08		M000644
			46A:D11
	M00063841A:B09		M000644
			57D:C09
	M00063886A:B06		M000644
			76D:C04
	M00063910D:A12		M000645
			06A:C07
	M00063912A:D06		M000645
			14A:G10
	M00063920D:H05		M000645
			20A:F08
	M00063928A:G09		M000645
			79D:E11
	M00063934B:E04		M000646
			20C:D01
	M00063945A:C03		M000646
			24D:C09
es77	M00064032D:G04	es81	M000646
			33C:A03
	M00064046A:G02		M000646
			37B:F03
	M00064053C:G04		M000646
			90A:C04
	M00064053D:F02		M000646
			90A:C04
	M00064082A:A08		M000647
			14A:G03
	M00064089B:F09		M000647
			23D:H11
	M00064132B:B07		GKC1015
			4-1

M00064138A:F11

GKC1015

4-3

M00064161B:G04

M00064175B:B09

es78

M00064178C:C04

M00064179A:C04

M00064200D:E08

M00064248A:E02

M00064270B:B03

M00064271B:D03

M00063580C:A06

M00063594B:H07

M00064002C:F06

M00064002C:H09

es82

M00063151A:G06

M00063852D:F07

M00063151D:B10

M00063888D:D05

M00063152C:B07

M00063888D:F02

M00063156D:H10

M00063890A:F11

M00063158A:E11

M00063890A:H04

M00063158A:E11

M00063891A:F11

M00063452A:F08

M00063892B:G02

M00063453B:F08

M00063898A:A10

M00063462D:D07

M00063915C:E01

M00063463D:B05

M00063919C:E07

M00063466C:C11

M00063920D:H02

M00063467D:H07

M00063922B:A12

M00063478C:D01

M00063925B:F04

M00063482A:A08

M00063926A:H04

M00063482A:F07

M00063931B:E10

M00063485A:E05

M00063931B:F07

M00063487C:C02

M00063932D:G08

M00063514C:D03

M00063934C:C10

M00063514C:E08

M00063938B:H07

M00063515B:F06

M00063939C:D06

M00063515B:H02

M00063939C:H01

M00063518D:A01

M00063940D:F09

M00063520D:D08

M00063940D:F09

M00063604A:B11

M00063941B:C12

M00063606C:B04

M00063943B:G12

M00063610D:C11

M00063949D:A05

M00063613D:C11

M00064021D:H01

M00063617D:F09

M00064025D:E07

M00063627C:F06

M00064025D:H12

M00063636A:E01

M00064033C:C11

M00063681B:C02	M00064033D:B01
M00063682A:C04	M00063843B:D07
M00063685A:C02	M00063848C:G11
M00063774A:D09	M00063852B:D08
M00063784A:H12	M00063818C:A09
M00063784C:E10	M00063828A:H12
M00063785C:F03	M00063828D:E05
M00063795C:D09	M00063839A:F01
M00063801B:D04	M00063841A:E08
M00063804C:A11	
M00063805D:E05	
M00063807A:D12	
M00063810C:E03	

es83

M00064043D:C09	M00063577C:C02
M00064048C:G12	M00063578B:E02
M00064053B:D09	M00063578C:A06
M00064057C:H10	M00063580D:B06
M00064059A:C11	M00063593A:D03
M00064060B:D03	M00063600C:C09
M00064079C:A10	M00063955C:F07
M00064082D:D10	M00063955D:F05
M00064083D:E05	M00063956A:F05
M00064086C:E01	M00063957A:E02
M00064090C:A02	M00063957A:E02
M00064090D:D09	M00063967C:A12
M00064105B:A03	M00063967D:G02
M00064106C:G03	M00063968D:G08
M00064113B:C04	M00063972C:E10
M00064115B:E12	M00063978B:B06
M00064119B:H10	M00063981D:A06
M00064119C:D12	M00063990A:D05
M00064122C:B06	M00063990A:D05
M00064126C:C02	M00063997C:B12
M00064126C:F12	M00063998C:E09
M00064136C:D12	M00064000B:C03
M00064144D:A07	M00064001A:B03
M00064151B:C07	M00064005D:A08
M00064159A:H03	M00064008A:B01
M00064165A:B12	M00064009A:C01
M00064171D:E05	M00064014D:H05
M00064171D:E05	M00064018C:E07
M00064172C:A02	M00064293D:B12
M00064173B:E01	M00064294D:F01
M00064176D:H10	M00063557D:C07
M00064178B:A05	M00063559D:G03

M00064178B:A05	M00063571B:G03
M00064180A:G03	M00063575B:G02
M00064186C:B03	M00063555B:D01
M00064188B:G08	M00063533A:C12
M00064194C:D02	M00063534C:A02
M00064212D:E04	M00063538D:B01
M00064260C:E05	M00063539C:C11
M00064268D:G03	
M00064272C:G01	
M00063163A:G04	
M00063165A:C09	

es84	M00064307B:G02	M00064564A:C02
	M00064307C:G03	M00064568A:H06
	M00064310C:A10	M00064569B:A09
	M00064328B:H04	M00064569B:A09
	M00064328B:H09	M00064571C:C04
	M00064337D:F01	M00064577C:B120
	M00064341A:C02	M00064579A:C06
	M00064345A:A03	M00064593A:A05
	M00064346C:B09	M00064593D:C01
	M00064349D:H01	M00064601C:G07
	M00064352C:H01	M00064601D:B05
	M00064354A:A10	M00064605C:G05
	M00064358A:G03	M00064610D:H01
	M00064358C:D09	M00064620D:G05
	M00064375B:G07	M00064624C:B03
	M00064376A:A05	M00064631A:C07
	M00064385D:C11	M00064631A:C07
	M00064386B:C02	M00064631C:H11
	M00064386B:C02	M00064636B:A04
	M00064393B:H04	M00064649A:E04
	M00064399A:E01	M00064650B:B07
	M00064405B:C04	M00064652B:D09
	M00064406B:H06	M00064675C:E09
	M00064414D:D06	M00064678D:F05
	M00064415B:G03	M00064693D:F08
	M00064424B:C12	M00064723C:H04
	M00064428B:A12	M00064723D:H03
	M00064447B:A07	M00064723D:H03
	M00064447B:C06	M00003773D:H02
	M00064450C:E07	M00021929A:D03
	M00064452D:E11	M00043134A:A05
	M00064454A:H10	M00064534D:F06

M00064454C:B06 M00064550A:A07
 M00064460C:B01 M00064554D:A03
 M00064467B:D06 M00064526D:F05
 M00064481C:F03 M00064527A:H07
 M00064508A:B09 M00064530B:H02
 M00064514D:F11 M00064532D:G06
 M00064517B:F04 M00064520A:E04
 M00064517B:F10 M00064520A:E04
 M00064517C:F11 M00064524A:A09

Table 127

Table 8 Patient ID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopathology Grade	Local Invasion	Lymph node Met	Incidence Lymph node Met	Regional Lymph node Grade	Distant Met & Loc	Description Distant Met	Distant Met Grade	Comments
15	21	Ascending colon	4.0	T3	G2	extending into subserosal adipose tissue	positive	3/8	N1	negative		MX	invasive adenocarcinoma, moderately differentiated ; focal perineural invasion is seen
52	71	Ascending colon	9.0	T3	G3	Invasion through muscularis propria, subserosal involvement; ileocec. valve involvement	negative	0/12	N0	negative		M0	Hyperplastic polyp in appendix.
121	140	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving submucosa of urinary bladder	negative	0/34	N0	negative		M0	Perineural invasion; donut anastomosis negative. One tubulovillous and one tubular adenoma with no

Table 8 Patient ID	Path Report ID	Anatomica l Loc	Primary Tumor Size	Prima ry Tumo r Grade	Histo path Grade	Local Invasion	Lymphn ode Met	Incide nce Lymph hnode Met	Regional Lymphn ode Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
													high grade dyspla sia.
125	144	Cecum	6	T3	G2	Invasion through the muscularis propria into suserosal adipose tissue. Ileocecal junction.	negative	0/19	N0	negati ve		M0	patient history of metast atic melan oma
128	147	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into percolonic fat	positive	1/5	N1	negati ve		M0	
130	149	Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue	positive	10/24	N2	negati ve		M1	
133	152	Rectum	5.0	T3	G2	Invasion through muscularis propria into non- peritonealiz ed pericolic tissue; gross configurati on is annular.	negative	0/9	N0	negati ve		M0	Small separat e tubular adeno ma (0.4 cm)

Table 8 Patient ID	Path Report ID	Anatomica l Loc	Primary Tumor Size	Prima ry Tumo r Grade	Histo path Grade	Local Invasion	Lymphn ode Met	Incide nce Lymph hnode Met	Regional Lymphn ode Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
141	160	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolonic adipose tissue, but not through serosa. Arising from tubular adenoma.	positive	7/21	N2	positive (Liver)	adenoc arcino ma consist ant with primar y	M1	Perine ural invasi on identif ied adjace nt to metast atic adenoc arcino ma.
156	175	Hepatic flexure	3.8	T3	G2	Invasion through mucularis propria into subserosa/p ericolic adipose, no serosal involvement. Gross configuration annular.	positive	2/13	N1	negati ve		M0	Separa te tubolo villous and tubular adeno mas
228	247	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectoal adipose, and serosa	positive	1/8	N1	negati ve		MX	Hyper plastic polyps
264	283	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.	negative	0/10	N0	negati ve		M0	Tubul ovillo us adeno ma with high grade dyspla sia

Table 8 Patient ID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histo path Grade	Local Invasion	Lymph node Met	Incidence Lymph node Met	Regional Lymph node Grade	Distant Met & Loc	Description Distant Met	Dist Met Grade	Comment
266	285	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolonic adipose, extends to serosa.	negative	0/15	N1	positive (Mesenteric deposition)	0.4 cm, may represent lymph node completely replaced by tumor	MX	
268	287	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy	negative	0/12	N0	negative		M0	
278	297	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.	positive	7/10	N2	negative		M0	Descending colon polyps, no HGD or carcinoma identified..
295	314	Ascending colon	5.0	T3	G2	Invasion through muscularis propria into percolic adipose tissue.	negative	0/12	N0	negative		M0	Melanosis coli and diverticular disease.
339	358	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa	negative	0/6	N0	negative		M0	1 hyperplastic polyp identified

Table 8 Patient ID	Path Report ID	Anatomica l Loc	Primary Tumor Size	Prima ry Tumo r Grade	Histo path Grade	Local Invasion	Lymphn ode Met	Incide nce Lymph node Met	Regional Lymphn ode Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
341	360	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	negative	0/4	N0	negati ve		MX	
356	375	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.	negative	0/4	N0	negati ve		M0	
360	412	Ascending colon	4.3	T3	G2	Invasion thru muscularis propria to pericolonic fat	positive	1/5	N1	negati ve		M0	Two mucos al polyps
392	444	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.	positive	1/6	N1	positiv e (Liver)	Macro vesicul ar and microv esicula steatos is	M1	Tumor arising at prior ileocol ic surgic al anasto mosis.
393	445	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.	negative	0/21	N0	negati ve		M0	

Table 8 Patient ID	Path Report ID	Anatomica l Loc	Primary Tumor Size	Prima ry Tumo r Grade	Histo path Grade	Local Invasion	Lymphn ode Met	Incide nce Lymph node Met	Regional Lymphn ode Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
413	465	Ascending colon	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.	negative	0/7	N0	positive (Liver)	adenoc arcino ma in multip le slides	M1	redia gnosis of oophor ectom y path to metast atic colon cancer
505	383		7.5 cm max dim	T3	G2	Invasion through muscularis propria involving pericolonic adipose, serosal surface uninvolved	positive	2/17	N1	positive (Liver)	moder ately differ entiated adenoc arcino ma, consist ant with primar y	M1	Anato mical locatio n of primar y not notate d in report. Eviden ce of chronic colitis.
517	395	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolonic fat.	positive	6/6	N2	negati ve		M0	No mentio n of distan t met in report
534	553	Ascending colon	12	T3	G3	Invasion through the muscularis propria involving pericolonic fat. Serosa free of tumor.	negative	0/8	N0	negati ve		M0	Oment um with fibrosi s and fat necros is. Small bowel with acute and chronic serositi s, focal absces s and adhesi ons.

Table 8 Patient ID	Path Report ID	Anatomic Location	Primary Tumor Size	Primary Tumor Grade	Histo path Grade	Local Invasion	Lymph node Met	Incide nce Lymph node Met	Regional Lymph node Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
546	565	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending to serosa.	positive	6/12	N2	positive (Liver)	metastatic adenocarcinoma	M1	
577	596	Cecum	11.5	T3	G2	Invasion through the bowel wall, into suberosal adipose. Serosal surface free of tumor.	negative	0/58	N0	negative		M0	Appendix dilated and fibrotic, but not involved by tumor
695	714	Cecum	14	T3	G2	extending through bowel wall into serosal fat	negative	0/22	N0	negative		MX	tubular adenoma and hyperplastic polyps present, moderately differentiated adenoma with mucinous differentiation (% not stated)
784	803	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues	positive	5/17	N2	positive (Liver)		M1	invasive poorly differentiated adenosquamous carcinoma

Table 8 Patient ID	Path Report ID	Anatomica l Loc	Primary Tumor Size	Prima ry Tumo r Grade	Histo path Grade	Local Invasion	Lymphn ode Met	Incide nce Lymph node Met	Regional Lymphn ode Grade	Distan t Met & Loc	Descri p Distan t Met	Dist Met Grade	Com ment
786	805	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface	negative	0/12	N0	positiv e (Liver)		M1	moder ately differe ntiated invasi ve adenoc arcino ma
791	810	Ascending colon	5.8	T3	G3	through the muscularis propria into pericolic fat	positive	13/25	N2	positiv e (Liver)		M1	poorly differe ntiated invasi ve coloni c adenoc arcino ma
888	908	Ascending colon	2.0	T2	G1	into muscularis propria	positive	3/21	N0	positiv e (Liver)		M1	well- to moder ately- differe ntiated adenoc arcino ma; this patient has tumors of the ascend ing colon and the sigmoi d colon
889	909	Cecum	4.8	T3	G2	through muscularis propria int subserosal tissue	positive	1/4	N1	positiv e (Liver)		M1	moder ately differe ntiated adenoc arcino ma

The deposits described herein are provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The

5 sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by

reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

5 Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using
10 methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated
15 SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA
20 from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be
25 encompassed by the following claims.

Example 82: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

Candidate polynucleotides that may represent novel polynucleotides were obtained from cDNA libraries generated from selected cell lines and patient tissues. In order to
 5 obtain the candidate polynucleotides, mRNA was isolated from several selected cell lines and patient tissues, and used to construct cDNA libraries. The cells and tissues that served as sources for these cDNA libraries are summarized in Table 129 below.

Human colon cancer cell line Km12L4-A (Morikawa, et al., Cancer Research (1988) 48:6863) is derived from the KM12C cell line. The KM12C cell line (Morikawa et
 10 al. Cancer Res. (1988) 48:1943-1948), which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B2 surgical specimen (Morikawa et al. Cancer Res. (1988) 48:6863). The KM12L4-A is a highly metastatic subline derived from KM12C (Yeatman et al. Nucl. Acids. Res. (1995) 23:4007; Bao-Ling et al. Proc. Annu. Meet. Am. Assoc. Cancer. Res. (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g.,
 15 KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., supra; Radinsky et al. Clin. Cancer Res. (1995) 1:19; Yeatman et al., (1995) supra; Yeatman et al. Clin. Exp. Metastasis (1996) 14:246).

The MDA-MB-231 cell line (Brinkley et al. Cancer Res. (1980) 40:3118-3129) was originally isolated from pleural effusions (Cailleau, J. Natl. Cancer. Inst. (1974) 53:661), is
 20 of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic
 25 variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human breast and lung cancer (see, e.g., Chandrasekaran et al., Cancer Res. (1979) 39:870 (MDA-MB-231 and MCF-7); Gastpar et al., J Med Chem (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et al., Br J Cancer (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., Nucleic Acids Res (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al.,
 30 Int J Cancer (1987) 40:46 (UCP-3); Varki et al., Tumour Biol. (1990) 11:327; (MV-522 and UCP-3); Varki et al., Anticancer Res. (1990) 10:637; (MV-522); Kelner et al., Anticancer Res (1995) 15:867 (MV-522); and Zhang et al., Anticancer Drugs (1997) 8:696 (MV522)).

The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cell lines were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

Table 129. Description of cDNA Libraries

Library (lib #)	Description	Number of Clones in Library
0	Artificial library composed of deselected clones (clones with no associated variant or cluster)	673
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMEC) - bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMEC) - VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349
25	Normal Prostate Epithelium from Patient IF97-26811	279444

Library (lib #)	Description	Number of Clones in Library
26	Prostate Cancer Epithelium Gleason 3+3 Patient IF97-26811	269406
27	Normal Breast Epithelium from Patient 515	239494
28	Primary Breast tumor from Patient 515	259960
29	Lymph node metastasis from Patient 515	326786
30	Normal Prostate Epithelium from Chiron Patient ID 884	298431
31	Prostate Cancer Epithelium (Gleason 4+4) from Chiron Patient ID 884	331941

Characterization of sequences in the libraries

After using the software program Phred (ver 0.000925.c, Green and Weing., ©1993-2000) to select those polynucleotides having the best quality sequence, the polynucleotides were compared against the public databases to identify any homologous sequences. The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the BLASTX masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., Meth. Enzymol. 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams et al., eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie et al. Comput. Chem. (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relatively little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 8064 sequences listed as SEQ ID NOS 15991-22000 in the accompanying Sequence Listing and summarized in Table 130 (inserted prior to claims). Each identified polynucleotide represents sequence from at least a partial mRNA transcript.

Summary of polynucleotides of the invention

Table 130 (inserted prior to claims) provides a summary of polynucleotides isolated as described. Specifically, Table 130 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER"); 3) the Sequence Name assigned to each sequence; 3) the sequence name ("SEQ NAME") used as an internal identifier of the sequence; 4) the orientation of the sequence ("ORIENT") (either forward (F) or reverse (R)); 5) the name assigned to the clone from which the sequence was isolated ("CLONE ID"); and the name of the library from which the sequence was isolated ("LIBRARY"), where the notation indicates that name of the cell line or patient sample (e.g., UC2-NormColon indicates the sequence was isolated from normal colon tissue of the patient assigned the identification UC#2). Because at least some of the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides may represent different regions of the same mRNA transcript and the same gene and/or may be contained within the same clone. Thus, for example, if two or more SEQ ID NOS are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene

Example 83: Results of Public Database Search to Identify Function of Gene

Products

SEQ ID NOS: 15991-22000 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to
 5 search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs, available over the world wide at a site sponsored by the National Center for Biotechnology Information, which is supported by the National Library of Medicine and the National Institutes of Health (see also Altschul, et al. Nucleic
 10 Acids Res. (1997) 25:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the BLASTX program for masking low complexity as described above in Example 82.

Tables 131A and 131B (inserted prior to claims) provides the alignment summaries having a p value of 1×10^{-2} or less indicating substantial homology between the
 15 sequences of the present invention and those of the indicated public databases. Specifically, Table 131A provides the SEQ ID NO of the query sequence, the accession number of the GenBank database entry of the homologous sequence, and the individual p value of each alignment. Table 131A provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous
 20 sequence, and the individual p value of each alignment. The alignments provided in Tables 131A and 131B are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification. The activity of the polypeptide encoded by the SEQ ID NOS listed in these tables can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related
 25 sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and
 30 actual activities and functions of the nearest neighbor sequences listed in Tables 131A and 131B and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the corresponding

5 polynucleotides.

Example 83.5:Members of Protein Families

SEQ ID NOS:15991-22000 were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table 132 (inserted before claims) provides the SEQ ID NO: of the query sequence, the Sequence Name, the Cluster to which the sequence is assigned, a brief description of the profile hit, the orientation (Direction, "Dir") of the query sequence with respect to the individual sequence)where forward (for) indicates that the alignment is in the same direction (left to right) as the sequence provided in the Sequence Listing and reverse (rev) indicates that the alignment is with a sequence complementary to the sequence provided in the Sequence Listing), and the score of the profile hit.

Some polynucleotides exhibited multiple profile hits where the query sequence contains overlapping profile regions, and/or where the sequence contains two different functional domains. Each of the profile hits of Table 132 is described in more detail below.

The acronyms for the profiles (provided in parentheses) are those used to identify the profile in the Pfam, Prosite, and InterPro databases. The Pfam database can be accessed through web sites supported by Genome Sequencing Center at the Washington University School of Medicine or by the European Molecular Biology Laboratories in Heidelberg, Germany. The Prosite database can be accessed at the ExPASy Molecular Biology Server on the internet. The InterPro database can be accessed at a web site supported by the EMBL European Bioinformatics Institute. The public information available on the Pfam, Prosite, and InterPro databases regarding the various profiles, including but not limited to the activities, function, and consensus sequences of various proteins families and protein domains, is incorporated herein by reference. **Table 132**

SEQ ID NO	SEQ NAME	CLUSTER	PROFILE NAME	DIR	SCOR E
15996	2102.B18.gz43_275316	558147	Ets_Cterm	for	19.58
15999	2103.M06.gz43_275519	377696	protkinase	for	20.71
16028	2153.K14.gz43_278937	372952	Dead_box_helic	for	172.21
16029	2154.M04.gz43_279163	377696	protkinase	for	20.71
16051	2165.H06.gz43_280342	393635	zf-c2h2	for	33.96

16059	2166.J11.gz43_281368	377696	protkinase	for	20.71
16098	2118.A09.gz43_307025	446397	bzip	for	19.15
16107	2131.I13.gz43_308085	34071	wd40	for	37.45
16108	2131.B14.gz43_308094	221686	protkinase	for	33.14
16218	1573.F18.gz43_208848	639849	PH	for	42.77
16219	1573.K19.gz43_208869	486238	protkinase	rev	45.41
16405	1585.G22.gz43_210545	412416	Dead_box_helic	for	49.67
16435	1587.B06.gz43_211440	446984	ANK	rev	23.12
16476	1597.G06.gz43_212233	639593	defensins	rev	18.27
16477	1597.J06.gz43_212236	557975	ANK	for	35.63
16492	1597.F18.gz43_212424	596882	zf-c2h2	rev	18.13
16690	1694.M19.gz43_214375	425923	zf-c2h2	for	32.76
16837	1706.P07.gz43_216138	639901	zf-c2h2	for	19.43
16867	1707.J02.gz43_216453	550237	zf-ccch	for	26.74
17501	1755.P24.gz43_223395	606129	rvt	for	37.6
17704	1790.C14.gz43_226997	727150	bzip	for	24.2
18024	1828.J19.gz43_232472	728303	zf-c2h2	rev	18.19
18028	1828.P21.gz43_232510	509678	Retvir_asp_protea se	for	28.5
18044	1838.N05.gz43_233020	481614	zf-c2h2	for	18.52
18504	1888.O06.gz43_240269	451764	rvt	for	49.99
18963	1924.H18.gz43_245579	499700	7tm_1	rev	73.7
19003	1935.E18.gz43_246500	490805	ANK	rev	28.74
19130	1981.O19.gz43_248062	558949	zf-c3hc4	rev	19.16
19393	1958.N12.gz43_250647	556308	zf-c2h2	for	40.77
19514	1923.M22.gz43_252963	562603	zf-c2h2	rev	42.42
19643	1995.C03.gz43_256117	562152	zf-c2h2	rev	18.97
19679	1995.P13.gz43_256290	562989	EGF	rev	19.4
19713	1995.B24.gz43_256452	556632	zf-c2h2	rev	20.64
19804	2007.F09.gz43_257778	560652	zf-c2hc	rev	21.49
19921	2008.F18.gz43_258308	550497	bzip	for	20.27
20141	1669.G11.gz43_260853	503275	protkinase	rev	43.25
20346	1682.O17.gz43_262495	450211	bzip	rev	26.06
20363	1682.F21.gz43_262550	546740	EFhand	rev	18.72
20678	2018.K14.gz43_264760	432970	zf-c2h2	for	48.43

20969	2041.C09.gz43_266976	556632	zf-c2h2	rev	20.88
21457	2067.I20.gz43_271090	551617	7tm_1	rev	19.77
21498	2068.F14.gz43_271375	561707	7tm_1	rev	24.27
21512	2068.D17.gz43_271421	554774	tgf-beta	for	18.24
21746	2176.J17.gz43_281945	412416	Dead_box_helic	for	37.64
21991	1561.C22.gz43_314731	447072	PH	for	31.95

Example 84: Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention were assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 129 above provides a summary of these libraries, including the shortened library name, the mRNA source used to prepared the cDNA library, the "nickname" of the library that is used in the tables below (in quotes), and the approximate number of clones in the library.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same

cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3, more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences Between Proportions," pp 296-298 (1974)).

Using this approach, a number of polynucleotide sequences were identified as being differentially expressed between, for example, cells derived from high metastatic potential cancer tissue and low metastatic cancer cells, and between cells derived from metastatic cancer tissue and normal tissue. Evaluation of the levels of expression of the genes corresponding to these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes corresponding to differentially expressed sequences described herein can be therapeutic targets due to their involvement in regulation (*e.g.*, inhibition or promotion) of development of, for example, the metastatic phenotype. For example,

sequences that correspond to genes that are increased in expression in high metastatic potential cells relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

5 Detection of the relative expression levels of differentially expressed polynucleotides described herein can provide valuable information to guide the clinician in the choice of therapy. For example, a patient sample exhibiting an expression level of one or more of these polynucleotides that corresponds to a gene that is increased in expression in metastatic or high metastatic potential cells may warrant more aggressive treatment for
10 the patient. In contrast, detection of expression levels of a polynucleotide sequence that corresponds to expression levels associated with that of low metastatic potential cells may warrant a more positive prognosis than the gross pathology would suggest.

 A number of polynucleotide sequences of the present invention are differentially expressed between human microvascular endothelial cells (HMVEC) that have been treated
15 with growth factors relative to untreated HMVEC. Sequences that are differentially expressed between growth factor-treated HMVEC and untreated HMVEC can represent sequences encoding gene products involved in angiogenesis, metastasis (cell migration), and other development and oncogenic processes. For example, sequences that are more highly expressed in HMVEC treated with growth factors (such as bFGF or VEGF) relative
20 to untreated HMVEC can serve as drug targets for chemotherapeutics, *e.g.*, decreasing expression of such up-regulated genes or inhibiting the activity of the encoded gene product would serve to inhibit tumor cell angiogenesis. Detection of expression of these sequences in colon cancer tissue can be valuable in determining diagnostic, prognostic and/or treatment information associated with the prevention of achieving the malignant
25 state in these tissues, and can be important in risk assessment for a patient. A patient sample displaying an increased level of one or more of these polynucleotides may thus warrant closer attention or more frequent screening procedures to catch the malignant state as early as possible.

 The differential expression of the polynucleotides can thus be used as, for example,
30 diagnostic and/or prognostic markers, for risk assessment, patient treatment and the like. These polynucleotides can also be used in combination with other molecular and/or biochemical markers.

The differential expression data for polynucleotides of the invention that have been identified as being differentially expressed across various combinations of the libraries described above is summarized in Table 133 (inserted prior to the claims). Table 133 provides: 1) the Sequence Identification Number ("SEQ ID NO") assigned to the polynucleotide; 2) the cluster ("CLUSTER") to which the polynucleotide has been assigned as described above; 3) the library comparisons that resulted in identification of the polynucleotide as being differentially expressed ("PAIR AB"), where the cDNA libraries used are referenced by their library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("CLONES A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("CLONES B"); 6) the "RATIO PLUS" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "RATIO MINUS" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

Detection of expression of genes that correspond to the above polynucleotides may be of particular interest in diagnosis, prognosis, risk assessment, and monitoring of treatment. Furthermore, differential expression of a specific gene across multiple libraries can also be indicative of a gene whose expression is associated with, for example, suppression of the metastatic phenotype or with development of the cell toward a metastatic phenotype. For example, SEQ ID NO:19734 corresponds to a gene that is expressed at relatively higher levels in metastatized colon tumor than in normal colon tissue. Thus a relatively increased level of expression of the gene corresponding to SEQ ID NO: 19734 may be used as marker of a metastatic or pre-metastatic colon cels either alone or in combination with other markers.

Some polynucleotides exhibited similar differential expression trends in libraries of different tissue origin (see, *e.g.*, SEQ ID NO:17327). These data suggest that the differential expression patterns of some genes associated with development of tumors indicate a role for those genes that is non-specific to the tissue of origin.

Example 85: Detection of Differential Expression Using Arrays

mRNA isolated from samples of cancerous and normal colon tissue obtained from patients were analyzed to identify genes differentially expressed in cancerous and normal cells. Normal and cancerous cells collected from cryopreserved patient tissues were

isolated using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001).

Table 134 (inserted before the claims) provides information about each patient from which colon tissue samples were isolated, including: the Patient ID ("PT ID") and Path ReportID ({Path ID}), which are numbers assigned to the patient and the pathology reports for identification purposes; the group ("Grp") to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the primary tumor size ("Size"); the primary tumor grade ("Grade"); the identification of the histopathological grade ("Histo Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("LN Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Incidence Lymphnode Met"); the "Regional Lymphnode Grade"; the identification or detection of metastases to sites distant to the tumor and their location ("Dist Met & Loc"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Histopathology of all primary tumors indicated the tumor was adenocarcinoma except for Patient ID Nos. 130 (for which no information was provided), 392 (in which greater than 50% of the cells were mucinous carcinoma), and 784 (adenosquamous carcinoma). Extranodal extensions were described in three patients, Patient ID Nos. 784, 789, and 791. Lymphovascular invasion was described in Patient ID Nos. 128, 278, 517, 534, 784, 786, 789, 791, 890, and 892. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791. Table 135 (below) provides information about the patients from whom the prostate tissue was isolated.

Table 135. Prostate patient data.

Prostate Patient ID	Tumor Gleason Grade	Normal Prostate Description
96	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
282	4+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
286	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
294	3+4 Adenocarcinoma	Normal prostate; Benign hyperplasia
362	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
428	4+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
492	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
492	3+3 Adenocarcinoma	Normal prostate; Benign hyperplasia
493	3+4 Adenocarcinoma	Normal prostate; Benign hyperplasia

Prostate Patient ID	Tumor Gleason Grade	Normal Prostate Description
510	3+3 Adenocarcinoma	Normal Prostate; Benign hyperplasia

Identification of differentially expressed genes

cDNA probes were prepared from total RNA isolated from the patient cells described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, e.g., Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.

Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array.

Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. For polynucleotides described herein, the microarray spot contained a clone having a cDNA from which the sequence was derived. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8

test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample.

Table 136 (inserted before the claims) describes sequences present on the arrays. Table 136 includes: 1) the SEQ ID NO of the sequence of the polynucleotide; and 2) the Spot ID, which is a unique identifier for each spot containing target sequence of interest on all arrays used.

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot

was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

Table 136 (inserted before the claims) provides the results for gene products differentially expressed in the colon tumor samples relative to normal tissue samples. Table 136 includes: 1) the SEQ ID NO; 2) the spot identification number ("SpotID"); 3) the percentage of patients tested in which expression levels of the gene (as detected using the corresponding clone) was at least 2-fold greater in cancerous colon tissue (primary colon tumor) than in matched normal tissue ("Colon >2x T/N "); 4) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon ≤halfx T/N"); and 5) the colon number ratios, indicating the number of patients upon which the provided ratios was based.

Table 136

SEQ ID NO	SpotID	T/N Colon >2x	T/N Colon <halfx	T/N Colon Num Ratios
15996	43971	0.0	75.0	8.0
16021	40453	0.0	42.9	7.0
16030	40457	0.0	71.4	7.0
16034	46308	0.0	50.0	8.0
16040	45610	0.0	62.5	8.0

16060	42816	0.0	50.0	8.0
16062	44673	0.0	50.0	8.0
16064	42422	0.0	37.5	8.0
16067	43983	0.0	37.5	8.0
16071	44679	0.0	50.0	8.0
16074	42418	0.0	37.5	8.0
16123	39755	0.0	42.9	7.0
16129	44916	0.0	50.0	8.0
16137	45618	0.0	37.5	8.0
16139	44926	0.0	50.0	8.0
16142	44216	0.0	37.5	8.0
16143	38367	0.0	42.9	7.0
16148	38357	0.0	57.1	7.0
16151	41869	0.0	42.9	7.0
16152	43508	0.0	37.5	8.0
16154	38365	0.0	57.1	7.0
16156	39069	0.0	42.9	7.0
16161	39061	0.0	57.1	7.0
16170	39767	0.0	42.9	7.0
16174	43881	0.0	37.5	8.0
16176	43873	0.0	37.5	8.0
16185	39769	0.0	57.1	7.0
16186	39775	0.0	57.1	7.0
16187	46330	0.0	37.5	8.0
16188	42471	0.0	37.5	8.0
16190	41173	0.0	42.9	7.0
16192	42479	0.0	50.0	8.0
16206	39621	0.0	42.9	7.0
16207	46007	0.0	50.0	8.0
16208	46015	0.0	62.5	8.0
16215	45301	0.0	37.5	8.0
16218	45303	0.0	37.5	8.0
16240	41033	0.0	57.1	7.0
16250	41035	0.0	57.1	7.0
16258	41027	0.0	42.9	7.0

16264	41737	0.0	42.9	7.0
16291	39647	0.0	42.9	7.0
16297	38943	0.0	42.9	7.0
16299	38939	0.0	42.9	7.0
16305	44939	0.0	37.5	8.0
16314	42827	0.0	37.5	8.0
16316	38231	0.0	42.9	7.0
16324	42819	0.0	37.5	8.0
16342	43521	0.0	62.5	8.0
16348	45633	0.0	50.0	8.0
16354	44931	0.0	50.0	8.0
16355	45635	0.0	50.0	8.0
16356	46345	0.0	37.5	8.0
16380	44947	0.0	50.0	8.0
16381	44247	0.0	50.0	8.0
16393	43501	0.0	37.5	8.0
16396	43489	0.0	50.0	8.0
16397	44951	0.0	37.5	8.0
16403	41755	0.0	42.9	7.0
16410	43541	0.0	37.5	8.0
16414	44953	0.0	50.0	8.0
16416	46365	0.0	62.5	8.0
16422	44909	0.0	50.0	8.0
16425	38210	0.0	42.9	7.0
16433	38928	0.0	42.9	7.0
16434	44911	0.0	50.0	8.0
16436	46361	0.0	50.0	8.0
16440	39632	0.0	42.9	7.0
16442	39620	0.0	42.9	7.0
16445	46363	0.0	62.5	8.0
16448	41736	0.0	57.1	7.0
16454	38944	0.0	42.9	7.0
16457	45605	0.0	62.5	8.0
16458	45609	0.0	100.0	8.0
16461	38228	0.0	57.1	7.0

16462	41740	0.0	42.9	7.0
16466	41032	0.0	42.9	7.0
16470	39638	0.0	57.1	7.0
16472	41760	0.0	42.9	7.0
16480	41754	0.0	71.4	7.0
16486	39980	0.0	57.1	7.0
16487	46315	0.0	37.5	8.0
16497	40674	0.0	42.9	7.0
16499	38566	0.0	57.1	7.0
16509	38590	0.0	42.9	7.0
16529	42813	0.0	37.5	8.0
16544	43515	0.0	50.0	8.0
16548	41400	0.0	42.9	7.0
16550	40702	0.0	42.9	7.0
16553	40000	0.0	42.9	7.0
16563	38185	0.0	42.9	7.0
16572	39587	0.0	42.9	7.0
16577	44925	0.0	50.0	8.0
16582	39597	0.0	57.1	7.0
16583	39593	0.0	42.9	7.0
16593	38893	0.0	42.9	7.0
16596	42842	0.0	62.5	8.0
16597	43540	0.0	50.0	8.0
16601	42840	0.0	50.0	8.0
16604	43548	0.0	37.5	8.0
16607	43538	0.0	50.0	8.0
16608	46340	0.0	37.5	8.0
16634	39586	0.0	42.9	7.0
16641	45656	0.0	37.5	8.0
16644	44254	0.0	50.0	8.0
16645	45652	0.0	37.5	8.0
16656	46285	0.0	37.5	8.0
16657	40290	0.0	42.9	7.0
16658	40304	0.0	42.9	7.0
16670	39592	0.0	42.9	7.0

16672	44950	0.0	37.5	8.0
16681	45571	0.0	37.5	8.0
16692	45654	0.0	37.5	8.0
16693	45660	0.0	37.5	8.0
16695	40292	0.0	42.9	7.0
16701	40294	0.0	42.9	7.0
16712	46364	0.0	37.5	8.0
16714	38892	0.0	42.9	7.0
16723	40998	0.0	57.1	7.0
16726	40996	0.0	57.1	7.0
16728	41712	0.0	42.9	7.0
16747	38196	0.0	42.9	7.0
16763	44881	0.0	37.5	8.0
16766	39610	0.0	42.9	7.0
16780	41016	0.0	42.9	7.0
16783	39942	0.0	42.9	7.0
16785	41718	0.0	42.9	7.0
16788	39938	0.0	42.9	7.0
16791	46289	0.0	37.5	8.0
16794	41024	0.0	42.9	7.0
16797	38536	0.0	71.4	7.0
16800	39948	0.0	42.9	7.0
16806	39236	0.0	71.4	7.0
16808	38540	0.0	42.9	7.0
16810	41720	0.0	42.9	7.0
16811	41728	0.0	42.9	7.0
16821	46293	0.0	37.5	8.0
16833	41358	0.0	71.4	7.0
16836	39954	0.0	57.1	7.0
16840	41360	0.0	42.9	7.0
16854	38550	0.0	42.9	7.0
16856	38409	0.0	31.7	41.0
16858	40652	0.0	42.9	7.0
16871	42070	0.0	57.1	7.0
16873	42072	0.0	57.1	7.0

16874	42074	0.0	42.9	7.0
16876	40658	0.0	42.9	7.0
16879	41372	0.0	42.9	7.0
16885	40670	0.0	42.9	7.0
16895	38147	0.0	42.9	7.0
16905	39563	0.0	42.9	7.0
16906	38863	0.0	42.9	7.0
16908	38859	0.0	42.9	7.0
16927	40346	0.0	42.9	7.0
16931	41046	0.0	42.9	7.0
16935	45605	0.0	62.5	8.0
16936	40326	0.0	71.4	7.0
16938	40328	0.0	42.9	7.0
16940	41032	0.0	42.9	7.0
16945	40342	0.0	42.9	7.0
16950	41742	0.0	42.9	7.0
16952	41056	0.0	42.9	7.0
16962	43215	0.0	50.0	8.0
16964	43203	0.0	37.5	8.0
16965	42497	0.0	37.5	8.0
16971	42505	0.0	62.5	8.0
16974	43209	0.0	50.0	8.0
16975	38431	0.0	57.1	7.0
16976	24379	0.0	36.6	41.0
16979	43909	0.0	100.0	8.0
16981	41667	0.0	42.9	7.0
16982	40985	0.0	42.9	7.0
16986	38873	0.0	42.9	7.0
16988	38875	0.0	42.9	7.0
16989	40977	0.0	42.9	7.0
16991	38169	0.0	42.9	7.0
16995	40987	0.0	42.9	7.0
16996	40261	0.0	42.9	7.0
17000	39809	0.0	42.9	7.0
17005	40973	0.0	42.9	7.0

17006	39579	0.0	42.9	7.0
17008	40965	0.0	42.9	7.0
17014	40263	0.0	42.9	7.0
17016	39811	0.0	57.1	7.0
17018	40513	0.0	57.1	7.0
17021	39821	0.0	42.9	7.0
17022	38871	0.0	42.9	7.0
17028	38175	0.0	42.9	7.0
17043	40267	0.0	42.9	7.0
17044	40273	0.0	42.9	7.0
17047	40525	0.0	42.9	7.0
17054	41685	0.0	42.9	7.0
17056	40991	0.0	42.9	7.0
17057	41217	0.0	71.4	7.0
17062	39907	0.0	57.1	7.0
17066	41221	0.0	42.9	7.0
17075	42027	0.0	42.9	7.0
17096	41227	0.0	42.9	7.0
17102	41923	0.0	71.4	7.0
17104	41223	0.0	42.9	7.0
17114	38503	0.0	42.9	7.0
17120	41933	0.0	42.9	7.0
17122	40623	0.0	42.9	7.0
17125	38527	0.0	42.9	7.0
17128	39905	0.0	42.9	7.0
17131	40613	0.0	42.9	7.0
17132	40615	0.0	42.9	7.0
17136	39925	0.0	42.9	7.0
17137	41333	0.0	42.9	7.0
17142	40627	0.0	42.9	7.0
17143	41339	0.0	42.9	7.0
17147	39933	0.0	42.9	7.0
17149	40629	0.0	42.9	7.0
17156	42045	0.0	42.9	7.0
17157	39921	0.0	42.9	7.0

17160	40637	0.0	71.4	7.0
17171	42035	0.0	42.9	7.0
17176	43931	0.0	37.5	8.0
17179	46029	0.0	37.5	8.0
17183	42523	0.0	37.5	8.0
17189	39829	0.0	42.9	7.0
17193	43923	0.0	62.5	8.0
17196	43229	0.0	50.0	8.0
17198	44629	0.0	37.5	8.0
17210	43219	0.0	50.0	8.0
17212	39835	0.0	100.0	7.0
17221	40529	0.0	100.0	7.0
17224	43921	0.0	37.5	8.0
17228	45319	0.0	50.0	8.0
17231	45313	0.0	37.5	8.0
17235	44627	0.0	37.5	8.0
17236	44631	0.0	37.5	8.0
17240	40531	0.0	42.9	7.0
17245	46035	0.0	62.5	8.0
17260	41233	0.0	85.7	7.0
17264	40537	0.0	42.9	7.0
17270	44637	0.0	37.5	8.0
17271	45335	0.0	37.5	8.0
17280	40535	0.0	57.1	7.0
17282	41241	0.0	42.9	7.0
17283	41943	0.0	42.9	7.0
17301	41947	0.0	42.9	7.0
17372	38765	0.0	57.1	7.0
17382	39467	0.0	57.1	7.0
17388	42861	0.0	62.5	8.0
17389	43559	0.0	37.5	8.0
17391	38146	0.0	37.5	8.0
17392	43553	0.0	37.5	8.0
17398	43555	0.0	42.9	7.0
17402	39463	0.0	71.4	7.0

17403	43557	0.0	42.9	7.0
17405	40175	0.0	42.9	7.0
17408	40167	0.0	42.9	7.0
17412	40260	0.0	37.5	8.0
17419	44965	0.0	37.5	8.0
17420	44969	0.0	42.9	7.0
17422	44967	0.0	42.9	7.0
17432	40165	0.0	42.9	7.0
17436	44265	0.0	42.9	7.0
17438	38162	0.0	37.5	8.0
17440	41678	0.0	37.5	8.0
17442	40974	0.0	37.5	8.0
17444	41674	0.0	37.5	8.0
17448	46379	0.0	37.5	8.0
17453	41670	0.0	37.5	8.0
17457	42871	0.0	50.0	8.0
17462	38172	0.0	37.5	8.0
17464	44273	0.0	50.0	8.0
17465	44277	0.0	50.0	8.0
17466	43569	0.0	37.5	8.0
17473	38872	0.0	50.0	8.0
17476	43577	0.0	50.0	8.0
17482	39576	0.0	57.1	7.0
17483	44977	0.0	50.0	8.0
17491	39580	0.0	62.5	8.0
17492	45689	0.0	37.5	8.0
17493	44985	0.0	50.0	8.0
17494	45681	0.0	75.0	8.0
17497	39578	0.0	57.1	7.0
17498	40984	0.0	50.0	8.0
17500	39584	0.0	42.9	7.0
17502	40990	0.0	37.5	8.0
17504	46391	0.0	37.5	8.0
17506	41682	0.0	42.9	7.0
17516	38769	0.0	42.9	7.0

17520	44612	0.0	37.5	8.0
17522	44622	0.0	37.5	8.0
17538	39473	0.0	57.1	7.0
17540	42281	0.0	42.9	7.0
17543	45320	0.0	37.5	8.0
17544	39479	0.0	42.9	7.0
17550	42287	0.0	42.9	7.0
17551	45314	0.0	37.5	8.0
17552	45326	0.0	37.5	8.0
17557	42273	0.0	42.9	7.0
17558	43210	0.0	37.5	8.0
17563	43910	0.0	37.5	8.0
17565	42279	0.0	42.9	7.0
17574	46034	0.0	37.5	8.0
17575	43934	0.0	50.0	8.0
17576	43936	0.0	50.0	8.0
17577	44632	0.0	50.0	8.0
17578	43222	0.0	50.0	8.0
17579	40187	0.0	42.9	7.0
17580	44626	0.0	50.0	8.0
17587	44640	0.0	50.0	8.0
17589	43232	0.0	37.5	8.0
17591	43930	0.0	37.5	8.0
17593	44628	0.0	37.5	8.0
17599	44638	0.0	37.5	8.0
17600	45332	0.0	50.0	8.0
17601	46042	0.0	37.5	8.0
17603	43228	0.0	37.5	8.0
17605	43932	0.0	37.5	8.0
17609	40183	0.0	57.1	7.0
17613	44260	0.0	37.5	8.0
17618	43562	0.0	62.5	8.0
17622	43564	0.0	37.5	8.0
17624	45666	0.0	50.0	8.0
17626	44968	0.0	37.5	8.0

17628	42852	0.0	37.5	8.0
17632	44974	0.0	50.0	8.0
17635	41587	0.0	42.9	7.0
17636	44266	0.0	37.5	8.0
17637	44268	0.0	37.5	8.0
17638	44962	0.0	37.5	8.0
17643	44972	0.0	37.5	8.0
17644	45668	0.0	50.0	8.0
17652	41593	0.0	42.9	7.0
17654	45676	0.0	50.0	8.0
17657	42866	0.0	62.5	8.0
17659	44274	0.0	37.5	8.0
17663	42874	0.0	50.0	8.0
17665	42876	0.0	37.5	8.0
17669	42289	0.0	57.1	7.0
17671	42880	0.0	37.5	8.0
17672	43580	0.0	50.0	8.0
17676	46384	0.0	37.5	8.0
17679	45682	0.0	37.5	8.0
17688	46396	0.0	50.0	8.0
17693	38406	0.0	57.1	7.0
17695	44282	0.0	37.5	8.0
17696	46400	0.0	37.5	8.0
17707	46388	0.0	37.5	8.0
17712	38416	0.0	42.9	7.0
17717	42301	0.0	42.9	7.0
17718	44978	0.0	37.5	8.0
17719	42543	0.0	37.5	8.0
17722	42535	0.0	37.5	8.0
17723	45684	0.0	50.0	8.0
17727	44990	0.0	50.0	8.0
17728	45686	0.0	62.5	8.0
17729	46390	0.0	37.5	8.0
17730	42531	0.0	50.0	8.0
17736	43243	0.0	37.5	8.0

17737	43947	0.0	50.0	8.0
17739	46055	0.0	50.0	8.0
17743	44651	0.0	37.5	8.0
17746	45347	0.0	37.5	8.0
17747	42547	0.0	37.5	8.0
17748	39816	0.0	42.9	7.0
17750	44643	0.0	50.0	8.0
17753	42555	0.0	37.5	8.0
17754	39114	0.0	57.1	7.0
17760	43945	0.0	37.5	8.0
17761	44647	0.0	37.5	8.0
17766	45359	0.0	37.5	8.0
17767	42551	0.0	50.0	8.0
17771	46049	0.0	37.5	8.0
17775	42545	0.0	37.5	8.0
17777	43261	0.0	37.5	8.0
17778	44657	0.0	50.0	8.0
17783	43249	0.0	37.5	8.0
17784	43255	0.0	37.5	8.0
17786	43959	0.0	50.0	8.0
17787	40524	0.0	42.9	7.0
17791	40526	0.0	42.9	7.0
17798	43961	0.0	50.0	8.0
17804	44661	0.0	50.0	8.0
17806	40520	0.0	42.9	7.0
17809	46075	0.0	50.0	8.0
17811	46079	0.0	50.0	8.0
17812	45375	0.0	37.5	8.0
17813	41222	0.0	42.9	7.0
17816	45367	0.0	37.5	8.0
17817	46067	0.0	37.5	8.0
17821	41224	0.0	42.9	7.0
17824	41230	0.0	57.1	7.0
17826	39204	0.0	42.9	7.0
17835	38504	0.0	42.9	7.0

17840	40612	0.0	42.9	7.0
17841	40616	0.0	42.9	7.0
17844	40614	0.0	42.9	7.0
17845	40624	0.0	42.9	7.0
17849	39912	0.0	42.9	7.0
17851	39918	0.0	42.9	7.0
17858	39906	0.0	42.9	7.0
17860	38528	0.0	42.9	7.0
17865	39226	0.0	42.9	7.0
17875	38514	0.0	42.9	7.0
17878	38522	0.0	42.9	7.0
17881	39230	0.0	42.9	7.0
17882	39922	0.0	42.9	7.0
17888	39924	0.0	42.9	7.0
17896	39936	0.0	42.9	7.0
17897	40626	0.0	42.9	7.0
17903	41240	0.0	57.1	7.0
17906	40225	0.0	42.9	7.0
17912	41641	0.0	42.9	7.0
17917	42036	0.0	42.9	7.0
17919	41938	0.0	42.9	7.0
17922	40235	0.0	42.9	7.0
17925	38117	0.0	42.9	7.0
17934	40929	0.0	42.9	7.0
17936	41952	0.0	42.9	7.0
17939	39527	0.0	57.1	7.0
17940	39533	0.0	42.9	7.0
17944	41944	0.0	42.9	7.0
17947	42046	0.0	42.9	7.0
17953	41342	0.0	42.9	7.0
17954	39535	0.0	42.9	7.0
17959	40544	0.0	42.9	7.0
17960	38821	0.0	42.9	7.0
17961	40231	0.0	42.9	7.0
17962	41647	0.0	42.9	7.0

17963	41344	0.0	42.9	7.0
17967	38823	0.0	42.9	7.0
17970	40943	0.0	42.9	7.0
17978	38831	0.0	42.9	7.0
17980	38127	0.0	42.9	7.0
17982	42044	0.0	42.9	7.0
17997	40945	0.0	42.9	7.0
17998	40953	0.0	42.9	7.0
18003	38135	0.0	42.9	7.0
18005	40959	0.0	42.9	7.0
18012	40249	0.0	42.9	7.0
18024	39551	0.0	42.9	7.0
18026	40949	0.0	42.9	7.0
18028	41651	0.0	42.9	7.0
18032	38143	0.0	42.9	7.0
18033	38835	0.0	42.9	7.0
18035	38843	0.0	42.9	7.0
18050	41987	0.0	42.9	7.0
18058	40587	0.0	42.9	7.0
18062	39875	0.0	42.9	7.0
18066	40589	0.0	42.9	7.0
18067	38471	0.0	42.9	7.0
18069	38483	0.0	42.9	7.0
18071	41283	0.0	42.9	7.0
18110	39195	0.0	42.9	7.0
18111	39891	0.0	42.9	7.0
18115	39193	0.0	42.9	7.0
18120	39199	0.0	42.9	7.0
18148	40593	0.0	42.9	7.0
18153	40603	0.0	42.9	7.0
18167	42009	0.0	42.9	7.0
18175	39526	0.0	42.9	7.0
18177	39536	0.0	42.9	7.0
18183	40942	0.0	42.9	7.0
18185	38120	0.0	42.9	7.0

18189	40238	0.0	42.9	7.0
18192	40240	0.0	42.9	7.0
18194	39522	0.0	42.9	7.0
18196	39534	0.0	42.9	7.0
18198	42011	0.0	42.9	7.0
18204	42013	0.0	42.9	7.0
18214	38132	0.0	42.9	7.0
18219	40256	0.0	42.9	7.0
18225	42343	0.0	37.5	8.0
18226	43041	0.0	37.5	8.0
18227	38144	0.0	42.9	7.0
18229	39548	0.0	57.1	7.0
18233	38842	0.0	42.9	7.0
18237	38142	0.0	42.9	7.0
18240	38138	0.0	42.9	7.0
18247	39552	0.0	57.1	7.0
18253	39544	0.0	42.9	7.0
18260	41650	0.0	42.9	7.0
18261	40952	0.0	42.9	7.0
18262	41652	0.0	42.9	7.0
18268	38470	0.0	42.9	7.0
18269	40954	0.0	42.9	7.0
18278	43753	0.0	50.0	8.0
18280	39176	0.0	57.1	7.0
18283	39874	0.0	42.9	7.0
18284	40590	0.0	42.9	7.0
18290	40592	0.0	42.9	7.0
18294	41292	0.0	42.9	7.0
18302	39180	0.0	42.9	7.0
18304	41294	0.0	42.9	7.0
18313	39192	0.0	42.9	7.0
18316	39888	0.0	42.9	7.0
18317	40584	0.0	42.9	7.0
18318	41282	0.0	42.9	7.0
18319	41990	0.0	42.9	7.0

18326	39184	0.0	42.9	7.0
18328	44459	0.0	62.5	8.0
18330	40586	0.0	42.9	7.0
18331	41992	0.0	42.9	7.0
18332	44457	0.0	37.5	8.0
18335	40580	0.0	42.9	7.0
18336	39186	0.0	85.7	7.0
18337	43747	0.0	50.0	8.0
18339	41288	0.0	42.9	7.0
18340	41986	0.0	42.9	7.0
18342	38494	0.0	71.4	7.0
18343	39188	0.0	85.7	7.0
18344	41996	0.0	42.9	7.0
18349	40608	0.0	42.9	7.0
18354	45165	0.0	50.0	8.0
18357	41312	0.0	42.9	7.0
18358	39198	0.0	42.9	7.0
18360	41306	0.0	42.9	7.0
18361	39904	0.0	57.1	7.0
18364	45163	0.0	37.5	8.0
18366	42002	0.0	42.9	7.0
18370	41310	0.0	42.9	7.0
18373	39200	0.0	42.9	7.0
18376	42899	0.0	50.0	8.0
18378	45869	0.0	37.5	8.0
18380	42901	0.0	37.5	8.0
18383	45709	0.0	62.5	8.0
18390	42893	0.0	50.0	8.0
18394	43585	0.0	37.5	8.0
18398	43599	0.0	50.0	8.0
18402	43587	0.0	37.5	8.0
18403	44301	0.0	50.0	8.0
18404	46411	0.0	37.5	8.0
18405	42909	0.0	62.5	8.0
18412	42895	0.0	37.5	8.0

18413	44995	0.0	37.5	8.0
18414	42911	0.0	50.0	8.0
18416	45865	0.0	37.5	8.0
18419	42885	0.0	37.5	8.0
18422	42887	0.0	50.0	8.0
18424	45705	0.0	37.5	8.0
18429	42012	0.0	42.9	7.0
18432	43593	0.0	37.5	8.0
18438	42905	0.0	37.5	8.0
18439	44303	0.0	50.0	8.0
18446	45697	0.0	50.0	8.0
18458	44305	0.0	62.5	8.0
18459	43609	0.0	37.5	8.0
18461	45009	0.0	50.0	8.0
18465	44317	0.0	50.0	8.0
18466	45719	0.0	37.5	8.0
18467	43761	0.0	50.0	8.0
18468	46431	0.0	50.0	8.0
18470	44311	0.0	62.5	8.0
18473	45017	0.0	50.0	8.0
18474	46421	0.0	50.0	8.0
18475	44313	0.0	50.0	8.0
18477	45019	0.0	37.5	8.0
18479	46417	0.0	37.5	8.0
18481	46423	0.0	37.5	8.0
18486	45713	0.0	37.5	8.0
18488	46425	0.0	37.5	8.0
18490	45013	0.0	37.5	8.0
18492	44319	0.0	37.5	8.0
18493	45723	0.0	37.5	8.0
18494	46427	0.0	37.5	8.0
18495	42534	0.0	37.5	8.0
18501	43938	0.0	37.5	8.0
18506	43950	0.0	37.5	8.0
18507	45360	0.0	37.5	8.0

18508	43944	0.0	37.5	8.0
18514	45348	0.0	37.5	8.0
18517	46052	0.0	37.5	8.0
18522	43946	0.0	37.5	8.0
18524	43236	0.0	37.5	8.0
18529	44650	0.0	37.5	8.0
18531	43242	0.0	50.0	8.0
18534	43244	0.0	50.0	8.0
18539	46056	0.0	50.0	8.0
18540	42556	0.0	37.5	8.0
18541	43262	0.0	50.0	8.0
18545	45169	0.0	37.5	8.0
18550	42550	0.0	37.5	8.0
18553	42552	0.0	37.5	8.0
18554	43966	0.0	50.0	8.0
18571	43968	0.0	37.5	8.0
18572	42554	0.0	50.0	8.0
18581	44660	0.0	37.5	8.0
18582	45362	0.0	37.5	8.0
18586	45376	0.0	62.5	8.0
18591	45364	0.0	37.5	8.0
18594	45374	0.0	37.5	8.0
18595	46066	0.0	37.5	8.0
18598	45368	0.0	37.5	8.0
18599	46078	0.0	50.0	8.0
18603	44668	0.0	50.0	8.0
18604	45370	0.0	37.5	8.0
18609	43592	0.0	37.5	8.0
18610	45875	0.0	37.5	8.0
18611	46068	0.0	75.0	8.0
18613	42882	0.0	37.5	8.0
18619	43588	0.0	37.5	8.0
18628	44296	0.0	37.5	8.0
18629	43401	0.0	50.0	8.0
18631	44298	0.0	37.5	8.0

18632	45710	0.0	50.0	8.0
18636	45008	0.0	50.0	8.0
18637	42910	0.0	62.5	8.0
18638	43596	0.0	75.0	8.0
18639	45706	0.0	37.5	8.0
18645	46410	0.0	37.5	8.0
18648	44994	0.0	50.0	8.0
18652	45708	0.0	50.0	8.0
18656	46416	0.0	37.5	8.0
18657	42912	0.0	37.5	8.0
18661	42902	0.0	37.5	8.0
18663	44300	0.0	37.5	8.0
18666	42904	0.0	50.0	8.0
18667	43598	0.0	50.0	8.0
18676	42906	0.0	50.0	8.0
18678	42695	0.0	37.5	8.0
18679	46404	0.0	37.5	8.0
18680	42898	0.0	50.0	8.0
18684	45885	0.0	37.5	8.0
18693	42908	0.0	37.5	8.0
18694	44292	0.0	37.5	8.0
18700	46412	0.0	37.5	8.0
18701	44306	0.0	37.5	8.0
18703	43614	0.0	37.5	8.0
18705	43616	0.0	37.5	8.0
18708	43612	0.0	50.0	8.0
18716	43606	0.0	87.5	8.0
18717	43610	0.0	50.0	8.0
18719	43602	0.0	37.5	8.0
18722	45714	0.0	37.5	8.0
18723	43604	0.0	50.0	8.0
18729	45018	0.0	50.0	8.0
18745	45718	0.0	37.5	8.0
18802	46418	0.0	37.5	8.0
18875	46215	0.0	37.5	8.0

18956	45529	0.0	37.5	8.0
18973	46229	0.0	37.5	8.0
18974	45533	0.0	50.0	8.0
18996	43756	0.0	50.0	8.0
19001	43758	0.0	62.5	8.0
19072	46222	0.0	37.5	8.0
19083	46212	0.0	37.5	8.0
19119	42718	0.0	37.5	8.0
19135	42710	0.0	37.5	8.0
19166	43424	0.0	37.5	8.0
19183	44822	0.0	37.5	8.0
19201	44818	0.0	50.0	8.0
19235	45860	0.0	50.0	8.0
19247	45858	0.0	37.5	8.0
19258	42356	0.0	37.5	8.0
19259	42364	0.0	37.5	8.0
19268	45862	0.0	37.5	8.0
19286	43064	0.0	37.5	8.0
19326	45170	0.0	37.5	8.0
19329	43768	0.0	50.0	8.0
19346	43776	0.0	50.0	8.0
19349	45176	0.0	50.0	8.0
19378	42698	0.0	50.0	8.0
19383	45184	0.0	37.5	8.0
19395	45878	0.0	37.5	8.0
19402	45884	0.0	37.5	8.0
19428	46020	0.0	37.5	8.0
19429	46032	0.0	50.0	8.0
19432	46026	0.0	37.5	8.0
19433	42516	0.0	50.0	8.0
19447	44117	0.0	50.0	8.0
19453	42719	0.0	50.0	8.0
19504	43423	0.0	50.0	8.0
19565	46233	0.0	37.5	8.0
19585	43054	0.0	50.0	8.0

19586	42352	0.0	37.5	8.0
19595	43746	0.0	50.0	8.0
19603	42366	0.0	50.0	8.0
19640	40101	0.0	42.9	7.0
19646	39407	0.0	42.9	7.0
19688	38695	0.0	42.9	7.0
19692	40107	0.0	42.9	7.0
19701	39401	0.0	42.9	7.0
19706	39405	0.0	42.9	7.0
19713	38697	0.0	42.9	7.0
19826	42213	0.0	42.9	7.0
19860	38717	0.0	42.9	7.0
19871	38719	0.0	42.9	7.0
19909	38707	0.0	42.9	7.0
19924	38713	0.0	42.9	7.0
19945	39419	0.0	42.9	7.0
20018	42274	0.0	42.9	7.0
20029	38772	0.0	42.9	7.0
20031	42286	0.0	42.9	7.0
20035	38770	0.0	42.9	7.0
20045	42282	0.0	42.9	7.0
20049	42284	0.0	42.9	7.0
20087	38774	0.0	42.9	7.0
20114	40313	0.0	42.9	7.0
20121	45625	0.0	50.0	8.0
20127	41005	0.0	42.9	7.0
20130	38203	0.0	42.9	7.0
20135	46325	0.0	37.5	8.0
20136	39611	0.0	42.9	7.0
20137	40309	0.0	57.1	7.0
20143	45619	0.0	37.5	8.0
20153	41697	0.0	42.9	7.0
20156	38899	0.0	42.9	7.0
20160	38903	0.0	42.9	7.0
20161	41003	0.0	42.9	7.0

20163	40995	0.0	42.9	7.0
20165	46321	0.0	37.5	8.0
20167	41017	0.0	42.9	7.0
20172	42474	0.0	50.0	8.0
20185	42478	0.0	37.5	8.0
20187	41015	0.0	42.9	7.0
20202	41713	0.0	42.9	7.0
20204	42480	0.0	37.5	8.0
20207	43886	0.0	37.5	8.0
20218	43888	0.0	37.5	8.0
20230	44586	0.0	37.5	8.0
20242	43188	0.0	37.5	8.0
20244	45304	0.0	62.5	8.0
20253	45996	0.0	37.5	8.0
20265	46016	0.0	37.5	8.0
20267	43198	0.0	37.5	8.0
20269	44606	0.0	50.0	8.0
20272	42496	0.0	50.0	8.0
20275	43900	0.0	37.5	8.0
20276	44608	0.0	37.5	8.0
20278	43902	0.0	75.0	8.0
20280	46006	0.0	37.5	8.0
20283	43192	0.0	37.5	8.0
20286	42490	0.0	37.5	8.0
20289	43896	0.0	37.5	8.0
20295	42492	0.0	37.5	8.0
20297	46008	0.0	50.0	8.0
20307	39941	0.0	42.9	7.0
20314	42053	0.0	42.9	7.0
20331	38541	0.0	42.9	7.0
20333	42055	0.0	42.9	7.0
20340	39241	0.0	42.9	7.0
20361	40647	0.0	42.9	7.0
20374	41355	0.0	42.9	7.0
20376	39261	0.0	42.9	7.0

20385	39967	0.0	42.9	7.0
20387	38559	0.0	42.9	7.0
20390	40663	0.0	42.9	7.0
20393	40669	0.0	42.9	7.0
20398	39263	0.0	42.9	7.0
20411	44930	0.0	37.5	8.0
20414	42071	0.0	42.9	7.0
20415	45638	0.0	37.5	8.0
20418	44228	0.0	37.5	8.0
20419	41371	0.0	42.9	7.0
20424	45640	0.0	50.0	8.0
20425	44163	0.0	37.5	8.0
20426	44171	0.0	37.5	8.0
20429	42818	0.0	50.0	8.0
20430	45634	0.0	50.0	8.0
20431	45644	0.0	50.0	8.0
20437	43471	0.0	37.5	8.0
20438	43536	0.0	62.5	8.0
20443	44944	0.0	37.5	8.0
20444	45646	0.0	37.5	8.0
20447	44238	0.0	37.5	8.0
20448	44936	0.0	50.0	8.0
20451	44161	0.0	37.5	8.0
20459	44938	0.0	50.0	8.0
20460	45636	0.0	50.0	8.0
20467	44804	0.0	37.5	8.0
20473	44100	0.0	50.0	8.0
20534	46230	0.0	37.5	8.0
20537	45532	0.0	37.5	8.0
20547	45526	0.0	50.0	8.0
20563	45536	0.0	37.5	8.0
20583	41535	0.0	42.9	7.0
20584	40123	0.0	57.1	7.0
20590	41525	0.0	42.9	7.0
20601	40817	0.0	42.9	7.0

20610	40821	0.0	42.9	7.0
20619	41529	0.0	42.9	7.0
20622	40825	0.0	42.9	7.0
20635	41527	0.0	42.9	7.0
20686	41527	0.0	42.9	7.0
20708	40823	0.0	42.9	7.0
20717	38758	0.0	57.1	7.0
20719	42229	0.0	42.9	7.0
20733	38764	0.0	42.9	7.0
20744	42235	0.0	42.9	7.0
20758	42239	0.0	42.9	7.0
20825	39472	0.0	42.9	7.0
20912	40868	0.0	57.1	7.0
20928	40866	0.0	42.9	7.0
20940	41576	0.0	42.9	7.0
20968	40870	0.0	42.9	7.0
21055	39488	0.0	42.9	7.0
21107	40888	0.0	42.9	7.0
21130	40886	0.0	42.9	7.0
21140	40890	0.0	42.9	7.0
21155	41588	0.0	42.9	7.0
21176	41596	0.0	42.9	7.0
21218	42290	0.0	42.9	7.0
21242	43118	0.0	50.0	8.0
21290	43114	0.0	62.5	8.0
21331	45220	0.0	37.5	8.0
21350	44518	0.0	37.5	8.0
21529	43120	0.0	37.5	8.0
21549	43812	0.0	50.0	8.0
21586	43810	0.0	50.0	8.0
21633	45224	0.0	50.0	8.0
21639	45226	0.0	37.5	8.0
21655	45922	0.0	37.5	8.0
21661	43265	0.0	37.5	8.0
21691	42573	0.0	37.5	8.0

21714	45232	0.0	37.5	8.0
21742	41161	0.0	71.4	7.0
21753	41163	0.0	42.9	7.0
21802	44591	0.0	50.0	8.0
21805	43189	0.0	37.5	8.0
21807	45293	0.0	37.5	8.0
21808	42487	0.0	37.5	8.0
21811	43191	0.0	37.5	8.0
21815	38917	0.0	42.9	7.0
21819	38913	0.0	42.9	7.0
21826	41875	0.0	42.9	7.0
21827	45987	0.0	37.5	8.0
21837	45289	0.0	37.5	8.0
21838	45989	0.0	50.0	8.0
21969	44537	0.0	50.0	8.0
16070	44681	12.5	37.5	8.0
16076	43981	12.5	50.0	8.0
16068	44675	37.5	0.0	8.0
16094	42428	37.5	0.0	8.0
19238	45866	37.5	0.0	8.0
17843	39216	42.9	0.0	7.0
18039	41657	42.9	0.0	7.0
21138	40188	42.9	0.0	7.0
16006	44200	50.0	0.0	8.0
19609	43404	50.0	0.0	8.0
16590	42108	57.1	0.0	7.0
20674	40125	57.1	0.0	7.0
17581	44634	62.5	0.0	8.0
17508	46399	71.4	0.0	7.0
17968	38827	71.4	0.0	7.0
16007	44202	75.0	0.0	8.0
17965	41244	85.7	0.0	7.0
16108	43970	87.5	0.0	8.0
16104	43972	100.0	0.0	8.0

Table 137 below provides the data for differential expression analysis on the arrays using samples from metastasized colon tissue. In this example, the samples used for hybridization to sequences on the microarray were derived from the matched metastasized (MT) colon tissue and normal (N) colon tissues of the patients. Table 137 includes: 1) the SEQ ID NO; 2) the percentage of patients tested in which expression levels of the gene (as detected using the corresponding clone) was at least 2-fold greater in metastasized cancerous colon tissue (MT) than in matched normal tissue ("Colon>2x MT/N "); 5) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon <=halfx T/N"); and 8) the colon number ratios, indicating the number of patients upon which the provided ratios was based. The corresponding data with the same sequence of the colon tumor tissue versus matched normal colon tissue (T/N) are provided for convenience in comparison.

Table 137. Polynucleotides Corresponding to Differentially Expressed Genes in Metastasized Colon Cancer Tissue

SEQ ID NO	Colon MT/N >2x	Colon MT/N <halfx	Colon MT/N Num Ratios by Clone	Colon T/N >2x	Colon T/N <halfx	Colon T/N Num Ratios
16207	40.0	0.0	5.0	0.0	50.0	8.0
16314	0.0	40.0	5.0	0.0	37.5	8.0
17643	0.0	40.0	5.0	0.0	37.5	8.0
17962	40.0	0.0	5.0	0.0	42.9	7.0
18336	20.0	40.0	5.0	0.0	85.7	7.0
18342	20.0	80.0	5.0	0.0	71.4	7.0
18343	20.0	40.0	5.0	0.0	85.7	7.0
18637	0.0	40.0	5.0	0.0	62.5	8.0
21331	0.0	40.0	5.0	0.0	37.5	8.0

Table 138 below provides the data for differential expression analysis on the arrays using samples from matched cancerous and normal prostate tissue (PT/N). Table 138 includes: 1) the SEQ ID NO; 2) the percentage of patients tested in which expression levels of the gene (as detected using the corresponding clone) was at least 2-fold greater in metastasized cancerous prostate tissue (PT) than in matched normal tissue ("Colon>2x PT/N "); 3) the percentage of patients tested in which expression levels of the gene was less than or equal to one-half of the expression level in matched normal cells ("Colon <=halfx

PT/N"); and 4) the prostate PT/N number ratios, indicating the number of patients upon which the provided ratios was based. The corresponding data with the same sequences for the colon tumor versus normal (T/N) and metastasized colon tissue versus normal (MT/N) are provided for convenience in comparison.

Table 138. Polynucleotides Corresponding to Differentially Expressed Genes in Prostate Cancer Tissue

SEQ ID NO	Prostate (PT/N) >2x	Prostate (PT/N) <halfx	Prostate (PT/N) Num Ratios	Colon T/N >2x	Colon T/N <halfx	Colon T/N Num Ratios	Colon MT/N >2x	Colon MT/N <halfx	Colon MT/N Num Ratios
16129	11.1	33.3	9.0	0.0	50.0	8.0			
16480	37.5	12.5	8.0	0.0	71.4	7.0			
16619	33.3	11.1	9.0						
16634	12.5	37.5	8.0	0.0	42.9	7.0			
17664	33.3	0.0	9.0						
18336	37.5	25.0	8.0	0.0	85.7	7.0	20.0	40.0	5.0
18342	37.5	12.5	8.0	0.0	71.4	7.0	20.0	80.0	5.0
18410	22.2	33.3	9.0						
19286	33.3	0.0	9.0	0.0	37.5	8.0			

Example 86: Antisense Regulation of Gene Expression

- 5 The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells can be further analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

- Methods for analysis using antisense technology are well known in the art. For example, a number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target are designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh, RNature, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors considered when designing antisense oligonucleotides include: 1) the secondary structure of oligonucleotides; 2) the secondary structure of the target gene; 3) the specificity with no or minimum cross-hybridization to other expressed genes; 4) stability; 5) length and 6) terminal GC content. The antisense oligonucleotide is designed to so that it will hybridize to its target sequence under conditions of high stringency at physiological temperatures (*e.g.*, an optimal temperature for the cells in culture to provide for hybridization in the cell, *e.g.*, about 37°C), but with minimal formation of homodimers.

Once synthesized and quantitated, the oligomers are screened for efficiency of a transcript knock-out in a panel of cancer cell lines. The efficiency of the knock-out is determined by analyzing mRNA levels using lightcycler quantification. The oligomers that resulted in the highest level of transcript knock-out, wherein the level was at least about
 5 50%, preferably about 80-90%, up to 95% or more up to undetectable message, are selected for use in a cell-based proliferation assay, an anchorage independent growth assay, and an apoptosis assay.

For example, where the polynucleotide is identified as having a role in colon cancer, the ability of the corresponding designed antisense oligonucleotide to inhibit gene
 10 expression is tested through transfection into SW620 colon colorectal carcinoma cells. For each transfection mixture, a carrier molecule, preferably a lipitoid or cholesterol, is prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μ m PVDF membrane. The antisense or control oligonucleotide is then prepared to a working concentration of 100 μ M in sterile Millipore
 15 water. The oligonucleotide is further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 μ M, or approximately 20 μ g oligo/ml of OptiMEM™. In a separate microfuge tube, lipitoid or cholesterol, typically in the amount of about 1.5-2 nmol lipitoid/ μ g antisense oligonucleotide, is diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide is immediately added to the diluted
 20 lipitoid and mixed by pipetting up and down. Oligonucleotide is added to the cells to a final concentration of 30 nM.

The level of target mRNA that corresponds to a target gene of interest in the transfected cells is quantitated in the cancer cell lines using the Roche LightCycler™ real-time PCR machine. Values for the target mRNA are normalized versus an internal control
 25 (e.g., beta-actin). For each 20 μ l reaction, extracted RNA (generally 0.2-1 μ g total) is placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water added to a total volume of 12.5 μ l. To each tube 7.5 μ l of a buffer/enzyme mixture is added, which is prepared by mixing (in the order listed) 2.5 μ l H₂O, 2.0 μ l 10X reaction buffer, 10 μ l oligo dT (20 pmol), 1.0 μ l dNTP mix (10 mM each), 0.5 μ l RNAsin® (20u) (Ambion, Inc., Hialeah,
 30 FL), and 0.5 μ l MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents are mixed by pipetting up and down, and the reaction mixture incubated at 42°C for 1 hour. The contents of each tube are centrifuged prior to amplification.

An amplification mixture is prepared by mixing in the following order: 1X PCR buffer II, 3 mM MgCl₂, 140 μM each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H₂O to 20 μl. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X

concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene, OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the fluorescence from SYBR® Green increases. To each 20 μl aliquot of amplification mixture, 2 μl of template RT are added, and amplification carried out according to standard protocols.

The results can be expressed as the percent decrease in expression of the corresponding gene product relative to non-transfected cells, vehicle-only transfected (mock-transfected) cells, or cells transfected with reverse control oligonucleotides.

Example 87: Effect of Expression on Proliferation

The effect of gene expression on the inhibition of cell proliferation can be assessed in, for example, metastatic breast cancer cell lines (MDA-MB-231 ("231")), SW620 colon colorectal carcinoma cells, or SKOV3 cells (a human ovarian carcinoma cell line).

Cells are plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide is diluted to 2 μM in OptiMEM™ and added to OptiMEM™ into which the delivery vehicle, lipitoid 116-6 in the case of SW620 cells or 1:1 lipitoid 1:cholesteroid 1 in the case of MDA-MB-231 cells, had been diluted. The oligo/delivery vehicle mixture is then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments was 300 nM, and the final ratio of oligo to delivery vehicle for all experiments is 1.5 nmol lipitoid/μg oligonucleotide.

Antisense oligonucleotides are prepared as described above (see Example 86). Cells are transfected overnight at 37°C and the transfection mixture replaced with fresh medium the next morning. Transfection is carried out as described above in Example 83.

Those antisense oligonucleotides that inhibit proliferation represent genes that play a role in production or maintenance of the cancerous phenotype.

Example 88: Effect of Gene Expression on Colony Formation

The effect of gene expression upon colony formation of, for example, SW620 cells, SKOV3 cells, and MD-MBA-231 cells can be tested in a soft agar assay. Soft agar assays are conducted by first establishing a bottom layer of 2 ml of 0.6% agar in media plated
 5 fresh within a few hours of layering on the cells. The cell layer is formed on the bottom layer by removing cells transfected as described above from plates using 0.05% trypsin and washing twice in media. The cells are counted in a Coulter counter, and resuspended to 10^6 per ml in media. 10 μ l aliquots are placed with media in 96-well plates (to check counting with WST1), or diluted further for the soft agar assay. 2000 cells are plated in 800 μ l 0.4%
 10 agar in duplicate wells above 0.6% agar bottom layer. After the cell layer agar solidifies, 2 ml of media is dribbled on top and antisense or reverse control oligo (produced as described in Example 86) added without delivery vehicles. Fresh media and oligos are added every 3-4 days. Colonies usually are expected to form in 10 days to 3 weeks. Fields of colonies are counted by eye. Wst-1 metabolism values can be used to compensate for
 15 small differences in starting cell number. Larger fields can be scanned for visual record of differences.

Those antisense oligonucleotides that inhibited colony formation represent genes that play a role in production or maintenance of the cancerous phenotype.

20 Example 89: Induction of Cell Death upon Depletion of Polypeptides by Depletion of mRNA ("Antisense Knockout")

In order to assess the effect of depletion of a target message upon cell death, SW620 cells, or other cells derived from a cancer of interest, are transfected for proliferation assays. For cytotoxic effect in the presence of cisplatin (cis), the same protocol is followed
 25 but cells are left in the presence of 2 μ M drug. Each day, cytotoxicity was monitored by measuring the amount of LDH enzyme released in the medium due to membrane damage. The activity of LDH is measured using the Cytotoxicity Detection Kit from Roche Molecular Biochemicals. The data is provided as a ratio of LDH released in the medium vs. the total LDH present in the well at the same time point and treatment (rLDH/tLDH).
 30 A positive control using antisense and reverse control oligonucleotides for BCL2 (a known anti-apoptotic gene) is included; loss of message for BCL2 leads to an increase in cell death compared with treatment with the control oligonucleotide (background cytotoxicity due to transfection).

Example 90: Functional Analysis of Gene Products Differentially Expressed in Cancer

The gene products of sequences of a gene differentially expressed in cancerous cells can be further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype. For example, the function of gene products corresponding to genes identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted or associated with a cell surface membrane, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype.

Where the gene product of the differentially expressed genes identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecules that inhibit or enhance function of the corresponding protein or protein family.

Additional functional assays include, but are not necessarily limited to, those that analyze the effect of expression of the corresponding gene upon cell cycle and cell migration. Methods for performing such assays are well known in the art.

Example 91: Contig Assembly and Additional Gene Characterization

The sequences of the polynucleotides provided in the present invention can be used to extend the sequence information of the gene to which the polynucleotides correspond (*e.g.*, a gene, or mRNA encoded by the gene, having a sequence of the polynucleotide described herein). This expanded sequence information can in turn be used to further characterize the corresponding gene, which in turn provides additional information about the nature of the gene product (*e.g.*, the normal function of the gene product). The additional information can serve to provide additional evidence of the gene product's use as a therapeutic target, and provide further guidance as to the types of agents that can modulate its activity.

For example, a contig can be assembled using the sequence of a polynucleotide described herein. A "contig" is a contiguous sequence of nucleotides that is assembled from nucleic acid sequences having overlapping (*e.g.*, shared or substantially similar) sequence information. The sequences of publicly-available ESTs (Expressed Sequence
5 Tags) and the sequences of various clones from several cDNA libraries synthesized at Chiron were used in the contig assembly. The contig is assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions. The resulting contig can then be used to search both the public databases as well as databases internal to the applicatns to matchthe polynucleotide contiged with homology data and/or
10 differential gene expressed data.

The sequence information obtained in the contig assembly described above can be used to obtain a consensus sequence derived from the contig using the Sequencher program. The consensus sequence can then be used as a query sequence in a BLASTN search of the DGTI DoubleTwist Gene Index (DoubleTwist, Inc., Oakland, CA), which
15 contains all the EST and non-redundant sequence in public databases. Alternatively, a sequence of a polynucleotide described herein can be used directly as a query sequence in a BLASTN search of the DGTI DoubleTwist Gene Index.

Through contig assembly and the use of homology searching software programs, the sequence information provided herein can be readily extended to confirm, or confirm a
20 predicted, gene having the sequence of the polynucleotides described in the present invention. Further the information obtained can be used to identify the function of the gene product of the gene corresponding to the polynucleotides described herein. While not necessary to the practice of the invention, identification of the function of the corresponding gene, can provide guidance in the design of therapeutics that target the gene
25 to modulate its activity and modulate the cancerous phenotype (*e.g.*, inhibit metastasis, proliferation, and the like).

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain
30 changes and modifications may be made thereto without departing from the spirit or scope of the appended claims. Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific

embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

Deposit Information.

A deposit of the biological materials in the tables referenced below was made with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, under the provisions of the Budapest Treaty, on or before the filing date of the present application. The accession number indicated is assigned after successful viability testing, and the requisite fees were paid. Access to said cultures will be available during pendency of the patent application to one determined by the Commissioner to be entitled to such under 37 C.F.R. §1.14 and 35 U.S.C. §122. All restriction on availability of said cultures to the public will be irrevocably removed upon the granting of a patent based upon the application. Moreover, the designated deposits will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit; or for the enforceable life of the U.S. patent, whichever is longer. Should a culture become nonviable or be inadvertently destroyed, or, in the case of plasmid-containing strains, lose its plasmid, it will be replaced with a viable culture(s) of the same taxonomic description.

These deposits are provided merely as a convenience to those of skill in the art, and are not an admission that a deposit is required. A license may be required to make, use, or sell the deposited materials, and no such license is hereby granted. The deposit below was received by the ATCC on or before the filing date of the present application.

Table 139. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 141 below provides the ATCC Accession Nos. of the ES deposits, all of which were deposited on or before June 13, 2000.

Table 140: Pools of Clones and Libraries Deposited with ATCC on or before June 13, 2000.

Library No.	CMCC No.	ATCC Accession No.	Library No.	CMCC No.	ATCC Accession No.
ES168	5276	PTA-2027	ES 189	5304	PTA-2052
ES169	5277	PTA-2028	ES 190	5305	PTA-2053

Library No.	CMCC No.	ATCC Accession No.	Library No.	CMCC No.	ATCC Accession No.
ES170	5284	PTA-2029	ES 191	5306	PTA-2054
ES171	5285	PTA-2030	ES 192	5307	PTA-2055
ES172	5286	PTA-2031	ES 193	5308	PTA-2056
ES173	5287	PTA-2032	ES 194	5309	PTA-2057
ES174	5288	PTA-2033	ES 195	5310	PTA-2058
ES175	5289	PTA-2034	ES 196	5311	PTA-2059
ES176	5290	PTA-2035	ES 197	5312	PTA-2060
ES177	5291	PTA-2036	ES 198	5313	PTA-2061
ES178	5292	PTA-2037	ES 199	5314	PTA-2062
ES179	5293	PTA-2038	ES 200	5315	PTA-2048
ES180	5294	PTA-2039	ES 201	5316	PTA-2049
ES181	5295	PTA-2040	ES 202	5317	PTA-2063
ES182	5296	PTA-2041	ES 203	5318	PTA-2064
ES183	5297	PTA-2042	ES 204	5319	PTA-2065
ES184	5298	PTA-2043	ES 205	5320	PTA-2066
ES185	5299	PTA-2044	ES 206	5321	PTA-2067
ES 186	5301	PTA-2045	ES 207	5322	PTA-2068
ES 187	5302	PTA-2046	ES 208	5253	PTA-2050
ES 188	5303	PTA-2047	ES 209	5324	PTA-2051

Table 141 (inserted before the claims) provides the clones in each of the above libraries.

- Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC
- 5 deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be
- 10 identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C
- 15 for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the
- 20 corresponding desired polynucleotide sequence.

Example 92: Source of Biological Materials and Overview of Novel Polynucleotides
Expressed by the Biological Materials

Candidate polynucleotides that may represent novel polynucleotides were obtained
5 from cDNA libraries generated from selected cell lines and patient tissues. In order to obtain
the candidate polynucleotides, mRNA was isolated from several selected cell lines and patient
tissues, and used to construct cDNA libraries. The cells and tissues that served as sources for
these cDNA libraries are summarized in Table 142 below.

Human colon cancer cell line Km12L4-A (Morikawa, et al., Cancer Research (1988)
10 48:6863) is derived from the KM12C cell line. The KM12C cell line (Morikawa et al. Cancer
Res. (1988) 48:1943-1948), which is poorly metastatic (low metastatic) was established in
culture from a Dukes' stage B2 surgical specimen (Morikawa et al. Cancer Res. (1988)
48:6863). The KM12L4-A is a highly metastatic subline derived from KM12C (Yeatman et
al. Nucl. Acids. Res. (1995) 23:4007; Bao-Ling et al. Proc. Annu. Meet. Am. Assoc. Cancer.
15 Res. (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-
A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see,
e.g., Moriakawa et al., supra; Radinsky et al. Clin. Cancer Res. (1995) 1:19; Yeatman et al.,
(1995) supra; Yeatman et al. Clin. Exp. Metastasis (1996) 14:246).

The MDA-MB-231 cell line (Brinkley et al. Cancer Res. (1980) 40:3118-3129) was
20 originally isolated from pleural effusions (Cailleau, J. Natl. Cancer. Inst. (1974) 53:661), is of
high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude
mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural
effusion of a breast adenocarcinoma and is non-metastatic. The MV-522 cell line is derived
from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low
25 metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3.
These cell lines are well-recognized in the art as models for the study of human breast and
lung cancer (see, e.g., Chandrasekaran et al., Cancer Res. (1979) 39:870 (MDA-MB-231 and
MCF-7); Gastpar et al., J Med Chem (1998) 41:4965 (MDA-MB-231 and MCF-7); Ranson et
al., Br J Cancer (1998) 77:1586 (MDA-MB-231 and MCF-7); Kuang et al., Nucleic Acids Res
30 (1998) 26:1116 (MDA-MB-231 and MCF-7); Varki et al., Int J Cancer (1987) 40:46 (UCP-3);
Varki et al., Tumour Biol. (1990) 11:327; (MV-522 and UCP-3); Varki et al., Anticancer Res.

(1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)).

The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation.

GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

The source materials for generating the normalized prostate libraries of libraries 25 and 26 were cryopreserved prostate tumor tissue from a patient with Gleason grade 3+3 adenocarcinoma and matched normal prostate biopsies from a pool of at-risk subjects under medical surveillance. The source materials for generating the normalized prostate libraries of libraries 30 and 31 were cryopreserved prostate tumor tissue from a patient with Gleason grade 4+4 adenocarcinoma and matched normal prostate biopsies from a pool of at-risk subjects under medical surveillance.

The source materials for generating the normalized breast libraries of libraries 27, 28 and 29 were cryopreserved breast tissue from a primary breast tumor (infiltrating ductal carcinoma)(library 28), from a lymph node metastasis (library 29), or matched normal breast biopsies from a pool of at-risk subjects under medical surveillance. In each case, prostate or breast epithelia were harvested directly from frozen sections of tissue by laser capture microdissection (LCM, Arcturus Engineering Inc., Mountain View, CA), carried out according to methods well known in the art (*see*, Simone et al. *Am J Pathol.* 156(2):445-52 (2000)), to provide substantially homogenous cell samples.

Table 142. Description of cDNA Libraries

Library (lib#)	Description	Number of Clones in Library
0	Artificial library composed of deselected clones (clones with no associated variant or cluster)	673
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771

Library (lib#)	Description	Number of Clones in Library
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMEC) - bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMEC) - VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	309349
25	Normal Prostate Epithelium from Patient IF97-26811	279444
26	Prostate Cancer Epithelium Gleason 3+3 Patient IF97-26811	269406
27	Normal Breast Epithelium from Patient 515	239494
28	Primary Breast tumor from Patient 515	259960
29	Lymph node metastasis from Patient 515	326786
30	Normal Prostate Epithelium from Chiron Patient ID 884	298431
31	Prostate Cancer Epithelium (Gleason 4+4) from Chiron Patient ID 884	331941

Characterization of sequences in the libraries

After using the software program Phred (ver 0.000925.c, Green and Weing., ©1993-2000) to select those polynucleotides having the best quality sequence, the polynucleotides were compared against the public databases to identify any homologous sequences. The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the RepeatMasker masking program, publicly available through a web site supported by the University of Washington (*See also* Smit, A.F.A. and Green, P., unpublished results). Generally, masking does not influence the final search results, except to eliminate sequences of relatively little interest due to their low complexity, and to eliminate multiple “hits” based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats.

The remaining sequences were then used in a homology search of the GenBank database using the TeraBLAST program (TimeLogic, Crystal Bay, Nevada). TeraBLAST is a version of the publicly available BLAST search algorithm developed by the National Center for Biotechnology, modified to operate at an accelerated speed with increased sensitivity on a specialized computer hardware platform. The program was run with the default parameters recommended by TimeLogic to provide the best sensitivity and speed for searching DNA and protein sequences. Sequences that exhibited greater than 70% overlap, 99% identity, and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a TeraBLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a TeraBLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of

human origin were also excluded. Second, a TeraBLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and
5 redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the sequences listed as SEQ ID NOS:22001-23267 in the accompanying Sequence Listing and summarized in Table 143 (inserted prior to claims). Each identified polynucleotide represents
10 sequence from at least a partial mRNA transcript.

Summary of polynucleotides of the invention

Table 143 (inserted prior to claims) provides a summary of polynucleotides isolated as described. Specifically, Table 143 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER");
15 3) the Sequence Name assigned to each sequence; 3) the sequence name ("SEQ NAME") used as an internal identifier of the sequence; 4) the orientation of the sequence ("ORIENT") (either forward (F) or reverse (R)); 5) the name assigned to the clone from which the sequence was isolated ("CLONE ID"); and 6) the name of the library from which the sequence was isolated ("LIBRARY"). Because at least some of the provided polynucleotides represent partial
20 mRNA transcripts, two or more polynucleotides may represent different regions of the same mRNA transcript and the same gene and/or may be contained within the same clone. Thus, for example, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene. Clones which comprise the sequences described herein were deposited as set out in the tables indicated below (see
25 Example entitled "Deposit Information").

Example 93: Contig Assembly

The sequences of the polynucleotides provided in the present invention can be used to extend the sequence information of the gene to which the polynucleotides correspond (e.g., a gene, or mRNA encoded by the gene, having a sequence of the polynucleotide described
30 herein). This expanded sequence information can in turn be used to further characterize the corresponding gene, which in turn provides additional information about the nature of the gene product (e.g., the normal function of the gene product). The additional information can serve

to provide additional evidence of the gene product's use as a therapeutic target, and provide further guidance as to the types of agents that can modulate its activity.

For example, a contig was assembled using the sequence of a polynucleotide described herein. A "contig" is a contiguous sequence of nucleotides that is assembled from nucleic acid sequences having overlapping (e.g., shared or substantially similar) sequence information. The sequences of publicly-available ESTs (Expressed Sequence Tags) and the sequences of various of the above-described polynucleotides were used in the contig assembly. The contig was assembled using the software program Sequencher, version 4.05, according to the manufacturer's instructions. The sequence information obtained in the contig assembly was then used to obtain a consensus sequence derived from the contig using the Sequencher program. The resulting consensus sequence was used to search both the public databases as well as databases internal to the applicants to match the consensus polynucleotide with homology data and/or differential gene expressed data.

The final result provided the sequences listed as SEQ ID NOS: 23268-23385 in the accompanying Sequence Listing and summarized in Table 144 (inserted prior to claims). Table 144 provides a summary of the consensus sequences assembled as described. Specifically, Table 144 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the consensus sequence name ("CONSENSUS SEQ NAME") used as an internal identifier of the sequence; and 3) the sequence name ("POLYNTD SEQ NAME") of a polynucleotide of SEQ ID NOS: 22001-23267 used in assembly of the consensus sequence.

Table 144

SEQ ID	CONSENSUS SEQ NAME	POLYNTD SEQ NAME
23268	Clu1009284.1	2490.J22.GZ43_363450
23269	Clu1022935.2	2561.O19.GZ43_376586
23270	Clu1037152.1	2558.L19.GZ43_374594
23271	Clu13903.1	2489.A13.GZ43_362841
23272	Clu139979.2	2504.B21.GZ43_365834
23273	Clu163602.2	2561.H17.GZ43_376416
23274	Clu187860.2	2474.P22.GZ43_361999
23275	Clu189993.1	2505.N19.GZ43_366504

23276	Clu20975.1	2466.F16.GZ43_360217
23277	Clu217122.1	2458.N10.GZ43_356930
23278	Clu218833.1	2562.O01.GZ43_375800
23279	Clu244504.2	2367.E23.GZ43_346113
23280	Clu271456.1	2365.G19.GZ43_345389
23281	Clu376516.1	2457.J23.GZ43_356451
23282	Clu376630.1	2467.B11.GZ43_360500
23283	Clu377044.2	2499.A22.GZ43_365257
23284	Clu379689.1	2540.M18.GZ43_372313
23285	Clu380482.2	2542.D09.GZ43_372856
23286	Clu387530.4	2475.N08.GZ43_362321
23287	Clu388450.2	2497.L05.GZ43_364736
23288	Clu396325.1	2561.P16.GZ43_376607
23289	Clu397115.3	2560.K18.GZ43_375337
23290	Clu398642.2	2542.N22.GZ43_373109
23291	Clu400258.1	2504.O12.GZ43_366137
23292	Clu402167.1	2540.C21.GZ43_372076
23293	Clu402591.3	2483.E11.GZ43_359762
23294	Clu402904.1	2504.J02.GZ43_366007
23295	Clu404081.2	2483.K02.GZ43_359897
23296	Clu411524.1	2497.C11.GZ43_364526
23297	Clu41346.1	2560.K08.GZ43_375327
23298	Clu415520.1	2561.L14.GZ43_376509
23299	Clu416124.1	2367.G17.GZ43_346155
23300	Clu417672.1	2367.I09.GZ43_346195
23301	Clu423664.1	2488.H12.GZ43_362624
23302	Clu429609.1	2457.M11.GZ43_356511
23303	Clu442923.3	2498.G15.GZ43_365010
23304	Clu446975.1	2459.K15.GZ43_357247
23305	Clu449839.2	2497.O09.GZ43_364812
23306	Clu449889.1	2475.N21.GZ43_362334
23307	Clu451707.2	2554.P16.GZ43_376223
23308	Clu454509.3	2542.M09.GZ43_373072
23309	Clu454796.1	2540.P02.GZ43_372369
23310	Clu455862.1	2560.I09.GZ43_375280

23311	Clu460493.1	2483.O07.GZ43_359998
23312	Clu464200.1	2465.G06.GZ43_358214
23313	Clu465446.2	2457.L21.GZ43_356497
23314	Clu470032.1	2474.C01.GZ43_361666
23315	Clu474125.1	2457.E23.GZ43_356331
23316	Clu474125.2	2541.A06.GZ43_372397
23317	Clu477271.1	2540.E17.GZ43_372120
23318	Clu480410.1	2498.H08.GZ43_365027
23319	Clu483211.2	2510.J18.GZ43_369259
23320	Clu497138.1	2458.N19.GZ43_356939
23321	Clu498886.1	2465.L22.GZ43_358350
23322	Clu498886.2	2541.B15.GZ43_372430
23323	Clu5013.2	2559.D05.GZ43_374772
23324	Clu5105.2	2542.D19.GZ43_372866
23325	Clu510539.2	2558.H17.GZ43_374496
23326	Clu514044.1	2367.F13.GZ43_346127
23327	Clu516526.1	2456.F23.GZ43_355971
23328	Clu519176.2	2559.H20.GZ43_374883
23329	Clu520370.1	2541.N01.GZ43_372704
23330	Clu524917.1	2464.H05.GZ43_357853
23331	Clu528957.1	2540.F15.GZ43_372142
23332	Clu533888.1	2557.L23.GZ43_374214
23333	Clu534076.1	2456.C05.GZ43_355881
23334	Clu540142.2	2456.H02.GZ43_355998
23335	Clu540379.2	2491.O02.GZ43_363934
23336	Clu549507.1	2483.B23.GZ43_359702
23337	Clu551338.3	2457.I12.GZ43_356416
23338	Clu552537.2	2540.C10.GZ43_372065
23339	Clu556827.3	2558.E24.GZ43_374431
23340	Clu558569.2	2558.D03.GZ43_374386
23341	Clu565709.1	2542.P02.GZ43_373137
23342	Clu568204.1	2456.M05.GZ43_356121
23343	Clu570804.1	2475.M20.GZ43_362309
23344	Clu572170.2	2557.H03.GZ43_374098
23345	Clu573764.1	2365.C10.GZ43_345284

23346	Clu587168.1	2483.F15.GZ43_359790
23347	Clu588996.1	2466.G06.GZ43_360231
23348	Clu597681.1	2459.A04.GZ43_356996
23349	Clu598388.1	2562.E03.GZ43_375562
23350	Clu604822.2	2504.F20.GZ43_365929
23351	Clu621573.1	2535.A08.GZ43_370095
23352	Clu625055.1	2511.A07.GZ43_369416
23353	Clu627263.1	2466.D20.GZ43_360173
23354	Clu635332.1	2480.D13.GZ43_358588
23355	Clu640911.2	2541.M24.GZ43_372703
23356	Clu641662.2	2555.D22.GZ43_373253
23357	Clu659483.1	2365.F12.GZ43_345358
23358	Clu6712.1	2535.P14.GZ43_370461
23359	Clu676448.3	2464.B01.GZ43_357705
23360	Clu682065.2	2467.E19.GZ43_360580
23361	Clu685244.2	2561.J01.GZ43_376448
23362	Clu691653.1	2560.O12.GZ43_375427
23363	Clu692282.1	2561.I11.GZ43_376434
23364	Clu697955.1	2557.J22.GZ43_374165
23365	Clu702885.3	2555.H18.GZ43_373345
23366	Clu70908.1	2561.C15.GZ43_376294
23367	Clu709796.2	2542.C20.GZ43_372843
23368	Clu715752.1	2459.A24.GZ43_357016
23369	Clu727966.1	2489.F09.GZ43_362957
23370	Clu732950.2	2475.L17.GZ43_362282
23371	Clu752623.2	2561.I07.GZ43_376430
23372	Clu756337.1	2561.I19.GZ43_376442
23373	Clu782981.1	2489.L05.GZ43_363097
23374	Clu805118.3	2480.D16.GZ43_358591
23375	Clu806992.2	2467.D20.GZ43_360557
23376	Clu823296.3	2558.P20.GZ43_374691
23377	Clu830453.2	2540.M22.GZ43_372317
23378	Clu839006.1	2507.H02.GZ43_367111
23379	Clu847088.1	2542.H23.GZ43_372966
23380	Clu853371.2	2491.I06.GZ43_363794

23381	Clu88462.1	2510.K15.GZ43_369280
23382	Clu935908.2	2505.O09.GZ43_366518
23383	Clu948383.1	2541.F05.GZ43_372516
23384	Clu966599.3	2507.L12.GZ43_367217
23385	Clu993554.1	2558.F19.GZ43_374450

Example 94: Additional Gene Characterization

Sequences of the polynucleotides of SEQ ID NOS: 22001-23267 were used as a query sequence in a TeraBLASTN search of the DoubleTwist Human Genome Sequence Database (DoubleTwist, Inc., Oakland, CA), which contains all the human genomic sequences that have been assembled into a contiguous model of the human genome. Predicted cDNA and protein sequences were obtained where a polynucleotide of the invention was homologous to a predicted full-length gene sequence. Alternatively, a sequence of a contig or consensus sequence described herein could be used directly as a query sequence in a TeraBLASTN search of the DoubleTwist Human Genome Sequence Database.

The final results of the search provided the predicted cDNA sequences listed as SEQ ID NOS: 1386-1477 in the accompanying Sequence Listing and summarized in Table 145 (inserted prior to claims), and the predicted protein sequences listed as SEQ ID NOS: 23478-23568 in the accompanying Sequence Listing and summarized in Table 146 (inserted prior to claims). Specifically, Table 145 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each cDNA sequence for use in the present specification; 2) the cDNA sequence name ("cDNA SEQ NAME") used as an internal identifier of the sequence; 3) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NO that maps to the cDNA; 4) The gene id number (GENE) of the DoubleTwist predicted gene; 5) the chromosome ("CHROM") containing the gene corresponding to the cDNA sequence; Table 146 provides: 1) the SEQ ID NO ("SEQ ID") assigned to each protein sequence for use in the present specification; 2) the protein sequence name ("PROTEIN SEQ NAME") used as an internal identifier of the sequence; 3) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NOS: 22001-23267 that maps to the protein sequence; 4) The gene id number (GENE) of the DoubleTwist predicted gene; 5) the chromosome ("CHROM") containing the gene corresponding to the cDNA sequence.

Table 145

SEQ ID	cDNA SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM
23386	DTT00087024.1	2467.H18.GZ43_360651	DTG00087008.1	1
23387	DTT00089020.1	2367.I15.GZ43_346201	DTG00089002.1	1
23388	DTT00171014.1	2473.F14.GZ43_361367	DTG00171001.1	1
23389	DTT00514029.1	2488.G02.GZ43_362590	DTG00514005.1	1
23390	DTT00740010.1	2466.I08.GZ43_360281	DTG00740003.1	1
23391	DTT00945030.1	2466.D19.GZ43_360172	DTG00945008.1	1
23392	DTT01169022.1	2464.N05.GZ43_357997	DTG01169003.1	2
23393	DTT01178009.1	2510.O21.GZ43_369382	DTG01178002.1	2
23394	DTT01315010.1	2496.F14.GZ43_364217	DTG01315001.1	2
23395	DTT01503016.1	2538.M17.GZ43_371544	DTG01503005.1	2
23396	DTT01555018.1	2538.C07.GZ43_371294	DTG01555002.1	2
23397	DTT01685047.1	2496.C08.GZ43_364139	DTG01685007.1	2
23398	DTT01764019.1	2535.C23.GZ43_370158	DTG01764003.1	2
23399	DTT01890015.1	2482.J06.GZ43_359493	DTG01890004.1	2
23400	DTT02243008.1	2474.J19.GZ43_361852	DTG02243002.1	3
23401	DTT02367007.1	2366.P08.GZ43_345738	DTG02367002.1	3
23402	DTT02671007.1	2464.H22.GZ43_357870	DTG02671002.1	3
23403	DTT02737017.1	2538.M16.GZ43_371543	DTG02737001.1	3
23404	DTT02850005.1	2472.G03.GZ43_360996	DTG02850001.1	3
23405	DTT02966016.1	2510.M14.GZ43_369327	DTG02966003.1	4
23406	DTT03037029.1	2504.D16.GZ43_365877	DTG03037005.1	4
23407	DTT03150008.1	2491.P10.GZ43_363966	DTG03150002.1	4
23408	DTT03367008.1	2542.P19.GZ43_373154	DTG03367003.1	4
23409	DTT03630013.1	2510.O22.GZ43_369383	DTG03630002.1	4
23410	DTT03881017.1	2507.O12.GZ43_367289	DTG03881007.1	5
23411	DTT03913023.1	2459.P24.GZ43_357376	DTG03913005.1	5
23412	DTT03978010.1	2367.G22.GZ43_346160	DTG03978001.1	5
23413	DTT04070014.1	2540.H07.GZ43_372182	DTG04070007.1	5
23414	DTT04084010.1	2542.D19.GZ43_372866	DTG04084001.1	5
23415	DTT04160007.1	2472.M22.GZ43_361159	DTG04160003.1	5
23416	DTT04302021.1	2483.O07.GZ43_359998	DTG04302002.1	5

23417	DTT04378009.1	2368.O11.GZ43_346725	DTG04378001.1	5
23418	DTT04403013.1	2506.M05.GZ43_366850	DTG04403003.1	5
23419	DTT04414015.1	2368.D20.GZ43_346470	DTG04414005.1	5
23420	DTT04660017.1	2507.C03.GZ43_366992	DTG04660003.1	6
23421	DTT04956054.1	2538.I17.GZ43_371448	DTG04956020.1	6
23422	DTT04970018.1	2365.F24.GZ43_345370	DTG04970007.1	6
23423	DTT05205007.1	2459.J12.GZ43_357220	DTG05205001.1	6
23424	DTT05571010.1	2555.J10.GZ43_373385	DTG05571004.1	7
23425	DTT05650008.1	2557.L01.GZ43_374192	DTG05650003.1	7
23426	DTT05742029.1	2560.K10.GZ43_375329	DTG05742002.1	7
23427	DTT06137030.1	2565.B15.GZ43_398171	DTG06137001.1	8
23428	DTT06161014.1	2367.F06.GZ43_346120	DTG06161007.1	8
23429	DTT06706019.1	2467.D10.GZ43_360547	DTG06706003.1	9
23430	DTT06837021.1	2540.I10.GZ43_372209	DTG06837002.1	9
23431	DTT07040015.1	2504.E23.GZ43_365908	DTG07040006.1	9
23432	DTT07088009.1	2565.H01.GZ43_397953	DTG07088001.1	9
23433	DTT07182014.1	2536.G22.GZ43_370637	DTG07182006.1	10
23434	DTT07405044.1	2560.B11.GZ43_375114	DTG07405010.1	10
23435	DTT07408020.1	2466.M02.GZ43_360371	DTG07408005.1	10
23436	DTT07498014.1	2506.K20.GZ43_366817	DTG07498002.1	10
23437	DTT07600010.1	2464.H17.GZ43_357865	DTG07600001.1	10
23438	DTT08005024.1	2475.N21.GZ43_362334	DTG08005009.1	11
23439	DTT08098020.1	2540.M18.GZ43_372313	DTG08098001.1	11
23440	DTT08167018.1	2542.F05.GZ43_372900	DTG08167002.1	11
23441	DTT08249022.1	2498.G15.GZ43_365010	DTG08249008.1	11
23442	DTT08499022.1	2540.A24.GZ43_372031	DTG08499009.1	12
23443	DTT08514022.1	2541.L12.GZ43_372667	DTG08514006.1	12
23444	DTT08527013.1	2489.F09.GZ43_362957	DTG08527005.1	12
23445	DTT08595020.1	2554.N09.GZ43_376168	DTG08595003.1	12
23446	DTT08711019.1	2540.C19.GZ43_372074	DTG08711001.1	12
23447	DTT08773020.1	2559.I12.GZ43_374899	DTG08773008.1	12
23448	DTT08874012.1	2537.P14.GZ43_371229	DTG08874001.1	12
23449	DTT09387018.1	2561.P19.GZ43_376610	DTG09387001.1	14
23450	DTT09396022.1	2489.M11.GZ43_363127	DTG09396001.1	14
23451	DTT09553027.1	2505.J22.GZ43_366411	DTG09553007.1	14

23452	DTT09604016.1	2483.J07.GZ43_359878	DTG09604006.1	14
23453	DTT09705033.1	2536.O22.GZ43_370829	DTG09705006.1	14
23454	DTT09742009.1	2542.N21.GZ43_373108	DTG09742002.1	15
23455	DTT09753017.1	2464.L02.GZ43_357946	DTG09753002.1	15
23456	DTT09793019.1	2464.I04.GZ43_357876	DTG09793004.1	15
23457	DTT09796028.1	2366.L21.GZ43_345942	DTG09796002.1	15
23458	DTT10221016.1	2556.C19.GZ43_373610	DTG10221004.1	16
23459	DTT10360040.1	2475.M20.GZ43_362309	DTG10360016.1	16
23460	DTT10539016.1	2506.J20.GZ43_366793	DTG10539005.1	17
23461	DTT10564022.1	2475.H06.GZ43_362175	DTG10564006.1	17
23462	DTT10683041.1	2542.K21.GZ43_373036	DTG10683007.1	17
23463	DTT10819011.1	2474.I06.GZ43_361815	DTG10819003.1	17
23464	DTT11363027.1	2542.C20.GZ43_372843	DTG11363008.1	19
23465	DTT11479018.1	2506.G24.GZ43_366725	DTG11479007.1	19
23466	DTT11483012.1	2459.H09.GZ43_357169	DTG11483001.1	19
23467	DTT11548015.1	2565.C17.GZ43_398204	DTG11548002.1	19
23468	DTT11730017.1	2535.B09.GZ43_370120	DTG11730004.1	20
23469	DTT11791010.1	2506.E12.GZ43_366665	DTG11791003.1	20
23470	DTT11864036.1	2456.H07.GZ43_356003	DTG11864011.1	21
23471	DTT11902028.1	2490.B06.GZ43_363242	DTG11902009.1	21
23472	DTT11915017.1	2474.G17.GZ43_361778	DTG11915002.1	21
23473	DTT11966040.1	2457.L21.GZ43_356497	DTG11966014.1	22
23474	DTT12042027.1	2459.G01.GZ43_357137	DTG12042005.1	22
23475	DTT12201062.1	2562.B09.GZ43_375496	DTG12201018.1	X
23476	DTT12470020.1	2489.A13.GZ43_362841	DTG12470004.1	X
23477	DTT12550009.1	2504.G01.GZ43_365934	DTG12550003.1	X

Table 146

SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ NAME	GENE	CHROM	DBL TWIST LOCUS ID
23478	DTP0008703 3.1	2467.H18.GZ43_36 0651	DTG00087008.1	1	DTL00087012.1
23479	DTP0008902 9.1	2367.I15.GZ43_346 201	DTG00089002.1	1	DTL00089002.1

23480	DTP0017102 3.1	2473.F14.GZ43_36 1367	DTG00171001.1	1	DTL00171013.1
23481	DTP0051403 8.1	2488.G02.GZ43_36 2590	DTG00514005.1	1	DTL00514023.1
23482	DTP0074001 9.1	2466.I08.GZ43_360 281	DTG00740003.1	1	DTL00740006.1
23483	DTP0094503 9.1	2466.D19.GZ43_36 0172	DTG00945008.1	1	
23484	DTP0116903 1.1	2464.N05.GZ43_35 7997	DTG01169003.1	2	DTL01169014.1
23485	DTP0117801 8.1	2510.O21.GZ43_36 9382	DTG01178002.1	2	DTL01178007.1
23486	DTP0131501 9.1	2496.F14.GZ43_36 4217	DTG01315001.1	2	DTL01315004.1
23487	DTP0150302 5.1	2538.M17.GZ43_37 1544	DTG01503005.1	2	DTL01503007.1
23488	DTP0155502 7.1	2538.C07.GZ43_37 1294	DTG01555002.1	2	DTL01555003.1
23489	DTP0168505 6.1	2496.C08.GZ43_36 4139	DTG01685007.1	2	DTL01685004.1
23490	DTP0176402 8.1	2535.C23.GZ43_37 0158	DTG01764003.1	2	DTL01764005.1
23491	DTP0189002 4.1	2482.J06.GZ43_359 493	DTG01890004.1	2	DTL01890001.1
23492	DTP0224301 7.1	2474.J19.GZ43_361 852	DTG02243002.1	3	DTL02243002.1
23493	DTP0236701 6.1	2366.P08.GZ43_34 5738	DTG02367002.1	3	DTL02367004.1
23494	DTP0267101 6.1	2464.H22.GZ43_35 7870	DTG02671002.1	3	DTL02671002.1
23495	DTP0273702 6.1	2538.M16.GZ43_37 1543	DTG02737001.1	3	DTL02737012.1
23496	DTP0285001 4.1	2472.G03.GZ43_36 0996	DTG02850001.1	3	DTL02850004.1
23497	DTP0296602 5.1	2510.M14.GZ43_36 9327	DTG02966003.1	4	DTL02966001.1

23498	DTP0303703 8.1	2504.D16.GZ43_36 5877	DTG03037005.1	4	DTL03037004.1
23499	DTP0315001 7.1	2491.P10.GZ43_36 3966	DTG03150002.1	4	DTL03149001.1
23500	DTP0336701 7.1	2542.P19.GZ43_37 3154	DTG03367003.1	4	DTL03367005.1
23501	DTP0363002 2.1	2510.O22.GZ43_36 9383	DTG03630002.1	4	DTL03630006.1
23502	DTP0388102 6.1	2507.O12.GZ43_36 7289	DTG03881007.1	5	DTL03881006.1
23503	DTP0391303 2.1	2459.P24.GZ43_35 7376	DTG03913005.1	5	DTL03913012.1
23504	DTP0397801 9.1	2367.G22.GZ43_34 6160	DTG03978001.1	5	DTL03978003.1
23505	DTP0407002 3.1	2540.H07.GZ43_37 2182	DTG04070007.1	5	
23506	DTP0408401 9.1	2542.D19.GZ43_37 2866	DTG04084001.1	5	DTL04084001.1
23507	DTP0416001 6.1	2472.M22.GZ43_36 1159	DTG04160003.1	5	DTL04160003.1
23508	DTP0430203 0.1	2483.O07.GZ43_35 9998	DTG04302002.1	5	DTL04302006.1
23509	DTP0437801 8.1	2368.O11.GZ43_34 6725	DTG04378001.1	5	
23510	DTP0440302 2.1	2506.M05.GZ43_36 6850	DTG04403003.1	5	DTL04403004.1
23511	DTP0441402 4.1	2368.D20.GZ43_34 6470	DTG04414005.1	5	DTL04414004.1
23512	DTP0466002 6.1	2507.C03.GZ43_36 6992	DTG04660003.1	6	DTL04660002.1
23513	DTP0495606 3.1	2538.I17.GZ43_371 448	DTG04956020.1	6	DTL04956028.1
23514	DTP0497002 7.1	2365.F24.GZ43_34 5370	DTG04970007.1	6	DTL04970008.1
23515	DTP0520501 6.1	2459.J12.GZ43_357 220	DTG05205001.1	6	DTL05205002.1

23516	DTP0557101 9.1	2555.J10.GZ43_373 385	DTG05571004.1	7	DTL05571003.1
23517	DTP0565001 7.1	2557.L01.GZ43_37 4192	DTG05650003.1	7	DTL05650004.1
23518	DTP0574203 8.1	2560.K10.GZ43_37 5329	DTG05742002.1	7	DTL05742003.1
23519	DTP0613703 9.1	2565.B15.GZ43_39 8171	DTG06137001.1	8	DTL06137003.1
23520	DTP0616102 3.1	2367.F06.GZ43_34 6120	DTG06161007.1	8	DTL06161006.1
23521	DTP0670602 8.1	2467.D10.GZ43_36 0547	DTG06706003.1	9	DTL06705001.1
23522	DTP0683703 0.1	2540.I10.GZ43_372 209	DTG06837002.1	9	DTL06837010.1
23523	DTP0704002 4.1	2504.E23.GZ43_36 5908	DTG07040006.1	9	DTL07040004.1
23524	DTP0708801 8.1	2565.H01.GZ43_39 7953	DTG07088001.1	9	DTL07088004.1
23525	DTP0740505 3.1	2560.B11.GZ43_37 5114	DTG07405010.1	10	DTL07405034.1
23526	DTP0740802 9.1	2466.M02.GZ43_36 0371	DTG07408005.1	10	DTL07408005.1
23527	DTP0749802 3.1	2506.K20.GZ43_36 6817	DTG07498002.1	10	DTL07498007.1
23528	DTP0760001 9.1	2464.H17.GZ43_35 7865	DTG07600001.1	10	DTL07600004.1
23529	DTP0800503 3.1	2475.N21.GZ43_36 2334	DTG08005009.1	11	DTL08005010.1
23530	DTP0809802 9.1	2540.M18.GZ43_37 2313	DTG08098001.1	11	DTL08098013.1
23531	DTP0816702 7.1	2542.F05.GZ43_37 2900	DTG08167002.1	11	DTL08167003.1
23532	DTP0824903 1.1	2498.G15.GZ43_36 5010	DTG08249008.1	11	DTL08249005.1
23533	DTP0849903 1.1	2540.A24.GZ43_37 2031	DTG08499009.1	12	DTL08499012.1

23534	DTP0851403 1.1	2541.L12.GZ43_37 2667	DTG08514006.1	12	DTL08514015.1
23535	DTP0852702 2.1	2489.F09.GZ43_36 2957	DTG08527005.1	12	DTL08527008.1
23536	DTP0859502 9.1	2554.N09.GZ43_37 6168	DTG08595003.1	12	DTL08595002.1
23537	DTP0871102 8.1	2540.C19.GZ43_37 2074	DTG08711001.1	12	DTL08710003.1
23538	DTP0877302 9.1	2559.I12.GZ43_374 899	DTG08773008.1	12	DTL08773011.1
23539	DTP0887402 1.1	2537.P14.GZ43_37 1229	DTG08874001.1	12	DTL08874009.1
23540	DTP0938702 7.1	2561.P19.GZ43_37 6610	DTG09387001.1	14	DTL09387002.1
23541	DTP0939603 1.1	2489.M11.GZ43_36 3127	DTG09396001.1	14	DTL09396016.1
23542	DTP0955303 6.1	2505.J22.GZ43_366 411	DTG09553007.1	14	DTL09553018.1
23543	DTP0960402 5.1	2483.J07.GZ43_359 878	DTG09604006.1	14	DTL09604010.1
23544	DTP0970504 2.1	2536.O22.GZ43_37 0829	DTG09705006.1	14	DTL09705005.1
23545	DTP0974201 8.1	2542.N21.GZ43_37 3108	DTG09742002.1	15	DTL09742007.1
23546	DTP0975302 6.1	2464.L02.GZ43_35 7946	DTG09753002.1	15	DTL09753011.1
23547	DTP0979302 8.1	2464.I04.GZ43_357 876	DTG09793004.1	15	DTL09793004.1
23548	DTP0979603 7.1	2366.L21.GZ43_34 5942	DTG09796002.1	15	DTL09796021.1
23549	DTP1022102 5.1	2556.C19.GZ43_37 3610	DTG10221004.1	16	DTL10221002.1
23550	DTP1036004 9.1	2475.M20.GZ43_36 2309	DTG10360016.1	16	DTL10360003.1
23551	DTP1053902 5.1	2506.J20.GZ43_366 793	DTG10539005.1	17	DTL10539004.1

23552	DTP1056403 1.1	2475.H06.GZ43_36 2175	DTG10564006.1	17	DTL10564006.1
23553	DTP1068305 0.1	2542.K21.GZ43_37 3036	DTG10683007.1	17	DTL10683002.1
23554	DTP1081902 0.1	2474.I06.GZ43_361 815	DTG10819003.1	17	DTL10819002.1
23555	DTP1136303 6.1	2542.C20.GZ43_37 2843	DTG11363008.1	19	DTL11363017.1
23556	DTP1147902 7.1	2506.G24.GZ43_36 6725	DTG11479007.1	19	DTL11479006.1
23557	DTP1148302 1.1	2459.H09.GZ43_35 7169	DTG11483001.1	19	DTL11483006.1
23558	DTP1154802 4.1	2565.C17.GZ43_39 8204	DTG11548002.1	19	DTL11548003.1
23559	DTP1173002 6.1	2535.B09.GZ43_37 0120	DTG11730004.1	20	DTL11730009.1
23560	DTP1179101 9.1	2506.E12.GZ43_36 6665	DTG11791003.1	20	DTL11791005.1
23561	DTP1186404 5.1	2456.H07.GZ43_35 6003	DTG11864011.1	21	DTL11864023.1
23562	DTP1190203 7.1	2490.B06.GZ43_36 3242	DTG11902009.1	21	DTL11902002.1
23563	DTP1191502 6.1	2474.G17.GZ43_36 1778	DTG11915002.1	21	DTL11915001.1
23564	DTP1196604 9.1	2457.L21.GZ43_35 6497	DTG11966014.1	22	DTL11966006.1
23565	DTP1204203 6.1	2459.G01.GZ43_35 7137	DTG12042005.1	22	DTL12042001.1
23566	DTP1220107 1.1	2562.B09.GZ43_37 5496	DTG12201018.1	X	DTL12201023.1
23567	DTP1247002 9.1	2489.A13.GZ43_36 2841	DTG12470004.1	X	DTL12470016.1
23568	DTP1255001 8.1	2504.G01.GZ43_36 5934	DTG12550003.1	X	DTL12550005.1

A correlation between the polynucleotide used as a query sequence as described above

and the corresponding predicted cDNA and protein sequences is contained in Table 147.

Specifically Table 147 provides: 1) the SEQ ID NO of the cDNA ("cDNA SEQ ID"); 2) the cDNA sequence name ("cDNA SEQ NAME") used as an internal identifier of the sequence; 3) the SEQ ID NO of the protein ("PROTEIN SEQ ID") encoded by the cDNA sequence 4) the sequence name of the protein ("PROTEIN SEQ NAME") encoded by the cDNA sequence; 5) the SEQ ID NO of the polynucleotide ("POLYNTD SEQ ID") of SEQ ID NOS: 22001-23267 that maps to the cDNA and protein; and 6) the sequence name ("POLYNTD SEQ NAME") of the polynucleotide of SEQ ID NOS: 22001-23267 that maps to the cDNA and protein.

Through contig and consensus sequence assembly and the use of homology searching software programs, the sequence information provided herein can be readily extended to confirm, or confirm a predicted, gene having the sequence of the polynucleotides described in the present invention. Further the information obtained can be used to identify the function of the gene product of the gene corresponding to the polynucleotides described herein. While not necessary to the practice of the invention, identification of the function of the corresponding gene, can provide guidance in the design of therapeutics that target the gene to modulate its activity and modulate the cancerous phenotype (*e.g.*, inhibit metastasis, proliferation, and the like).

Example 95: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:22001-23477 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to search for homologous sequences in the GenBank (nucleotide sequences) database. Query and individual sequences were aligned using the TeraBLAST program available from TimeLogic, Crystal Bay, Nevada. The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the RepeatMasker masking program for masking low complexity as described above.

Table 148 (inserted prior to claims) provides the alignment summaries having a p value of 1×10^{-2} or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Specifically, Table 148 provides: 1) the SEQ ID NO ("SEQ ID") of the query sequence; 2) the sequence name ("SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("ACCESSION") of the

GenBank database entry of the homologous sequence; 4) a description of the GenBank sequences ("GENBANK DESCRIPTION"); and 5) the score of the similarity of the polynucleotide sequence and the GenBank sequence ("GENBANK SCORE"). The alignments provided in Table 148 are the best available alignment to a DNA sequence at a time just prior to filing of the present specification. Also incorporated by reference is all publicly available information regarding the sequence listed in Table 147 and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated. Full length sequences or fragments of the polynucleotide sequences can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide.

Table 147

cDNA SEQ ID	cDNA SEQ NAME	PROTEIN SEQ ID	PROTEIN SEQ NAME	POLYNTD SEQ ID	POLYNTD SEQ NAME
23386	DTT00087024.1	1478	DTP00087033.1	963	2467.H18.GZ43_360651
23386	DTT00087024.1	1478	DTP00087033.1	33	2505.B05.GZ43_366202
23387	DTT00089020.1	1479	DTP00089029.1	213	2367.I15.GZ43_346201
23388	DTT00171014.1	1480	DTP00171023.1	1006	2473.F14.GZ43_361367
23388	DTT00171014.1	1480	DTP00171023.1	1122	2489.A03.GZ43_362831
23389	DTT00514029.1	1481	DTP00514038.1	1113	2488.G02.GZ43_362590
23390	DTT00740010.1	1482	DTP00740019.1	952	2466.I08.GZ43_360281
23391	DTT00945030.1	1483	DTP00945039.1	945	2466.D19.GZ43_360172
23392	DTT01169022.1	1484	DTP01169031.1	482	2540.I17.GZ43_372216
23392	DTT01169022.1	1484	DTP01169031.1	914	2464.N05.GZ43_357997
23393	DTT01178009.1	1485	DTP01178018.1	113	2510.O21.GZ43_369382
23394	DTT01315010.1	1486	DTP01315019.1	1181	2496.F14.GZ43_364217
23395	DTT01503016.1	1487	DTP01503025.1	386	2538.M17.GZ43_371544
23396	DTT01555018.1	1488	DTP01555027.1	366	2538.C07.GZ43_371294
23396	DTT01555018.1	1488	DTP01555027.1	368	2538.D03.GZ43_371314
23396	DTT01555018.1	1488	DTP01555027.1	369	2538.D04.GZ43_371315
23397	DTT01685047.1	1489	DTP01685056.1	1177	2496.C08.GZ43_364139
23398	DTT01764019.1	1490	DTP01764028.1	267	2535.C23.GZ43_370158
23398	DTT01764019.1	1490	DTP01764028.1	771	2456.D04.GZ43_355904
23399	DTT01890015.1	1491	DTP01890024.1	1087	2482.J06.GZ43_359493
23399	DTT01890015.1	1491	DTP01890024.1	1042	2475.B20.GZ43_362045

23399	DTT01890015.1	1491	DTP01890024.1	1200	2497.L21.GZ43_364752
23400	DTT02243008.1	1492	DTP02243017.1	1224	2562.G21.GZ43_375628
23400	DTT02243008.1	1492	DTP02243017.1	1204	2497.P04.GZ43_364831
23400	DTT02243008.1	1492	DTP02243017.1	1025	2474.J19.GZ43_361852
23400	DTT02243008.1	1492	DTP02243017.1	1191	2497.D11.GZ43_364550
23401	DTT02367007.1	1493	DTP02367016.1	174	2366.P08.GZ43_345738
23402	DTT02671007.1	1494	DTP02671016.1	903	2464.H22.GZ43_357870
23402	DTT02671007.1	1494	DTP02671016.1	1055	2480.G11.GZ43_358658
23403	DTT02737017.1	1495	DTP02737026.1	385	2538.M16.GZ43_371543
23404	DTT02850005.1	1496	DTP02850014.1	992	2472.G03.GZ43_360996
23404	DTT02850005.1	1496	DTP02850014.1	1111	2488.F06.GZ43_362570
23404	DTT02850005.1	1496	DTP02850014.1	1039	2475.N08.GZ43_362321
23405	DTT02966016.1	1497	DTP02966025.1	103	2510.M14.GZ43_369327
23406	DTT03037029.1	1498	DTP03037038.1	9	2504.D16.GZ43_365877
23407	DTT03150008.1	1499	DTP03150017.1	428	2565.G20.GZ43_398256
23407	DTT03150008.1	1499	DTP03150017.1	585	2555.I12.GZ43_373363
23407	DTT03150008.1	1499	DTP03150017.1	235	2368.D08.GZ43_346458
23407	DTT03150008.1	1499	DTP03150017.1	1174	2491.P10.GZ43_363966
23408	DTT03367008.1	1500	DTP03367017.1	519	2506.E18.GZ43_366671
23408	DTT03367008.1	1500	DTP03367017.1	557	2542.P19.GZ43_373154
23409	DTT03630013.1	1501	DTP03630022.1	114	2510.O22.GZ43_369383
23410	DTT03881017.1	1502	DTP03881026.1	1251	2507.O12.GZ43_367289
23411	DTT03913023.1	1503	DTP03913032.1	889	2459.P24.GZ43_357376
23412	DTT03978010.1	1504	DTP03978019.1	211	2367.G22.GZ43_346160
23413	DTT04070014.1	1505	DTP04070023.1	423	2565.D06.GZ43_398029
23413	DTT04070014.1	1505	DTP04070023.1	374	2538.F03.GZ43_371362
23413	DTT04070014.1	1505	DTP04070023.1	17	2504.I13.GZ43_365994
23413	DTT04070014.1	1505	DTP04070023.1	692	2559.K12.GZ43_374947
23413	DTT04070014.1	1505	DTP04070023.1	43	2505.E15.GZ43_366284
23413	DTT04070014.1	1505	DTP04070023.1	750	2561.M09.GZ43_376528
23413	DTT04070014.1	1505	DTP04070023.1	463	2540.H07.GZ43_372182
23413	DTT04070014.1	1505	DTP04070023.1	1069	2481.D13.GZ43_358972
23414	DTT04084010.1	1506	DTP04084019.1	543	2542.D19.GZ43_372866
23415	DTT04160007.1	1507	DTP04160016.1	999	2472.M22.GZ43_361159
23416	DTT04302021.1	1508	DTP04302030.1	1106	2483.O07.GZ43_359998

23417	DTT04378009.1	1509	DTP04378018.1	260	2368.O11.GZ43_346725
23418	DTT04403013.1	1510	DTP04403022.1	531	2506.M05.GZ43_366850
23419	DTT04414015.1	1511	DTP04414024.1	236	2368.D20.GZ43_346470
23420	DTT04660017.1	1512	DTP04660026.1	334	2537.D11.GZ43_370938
23420	DTT04660017.1	1512	DTP04660026.1	1244	2507.C03.GZ43_366992
23421	DTT04956054.1	1513	DTP04956063.1	379	2538.I17.GZ43_371448
23422	DTT04970018.1	1514	DTP04970027.1	363	2538.B03.GZ43_371266
23422	DTT04970018.1	1514	DTP04970027.1	259	2368.O03.GZ43_346717
23422	DTT04970018.1	1514	DTP04970027.1	1101	2483.K02.GZ43_359897
23422	DTT04970018.1	1514	DTP04970027.1	134	2365.F24.GZ43_345370
23423	DTT05205007.1	1515	DTP05205016.1	880	2459.J12.GZ43_357220
23424	DTT05571010.1	1516	DTP05571019.1	586	2555.J10.GZ43_373385
23425	DTT05650008.1	1517	DTP05650017.1	644	2557.L01.GZ43_374192
23426	DTT05742029.1	1518	DTP05742038.1	721	2560.K10.GZ43_375329
23426	DTT05742029.1	1518	DTP05742038.1	126	2365.D10.GZ43_345308
23426	DTT05742029.1	1518	DTP05742038.1	756	2561.I19.GZ43_376442
23427	DTT06137030.1	1519	DTP06137039.1	419	2565.B15.GZ43_398171
23428	DTT06161014.1	1520	DTP06161023.1	205	2367.F06.GZ43_346120
23429	DTT06706019.1	1521	DTP06706028.1	967	2467.D10.GZ43_360547
23430	DTT06837021.1	1522	DTP06837030.1	465	2540.I10.GZ43_372209
23431	DTT07040015.1	1523	DTP07040024.1	10	2504.E23.GZ43_365908
23432	DTT07088009.1	1524	DTP07088018.1	170	2366.J06.GZ43_345700
23432	DTT07088009.1	1524	DTP07088018.1	429	2565.H01.GZ43_397953
23433	DTT07182014.1		DTP07182023.1	306	2536.G22.GZ43_370637
23434	DTT07405044.1	1525	DTP07405053.1	703	2560.B11.GZ43_375114
23435	DTT07408020.1	1526	DTP07408029.1	956	2466.M02.GZ43_360371
23436	DTT07498014.1	1527	DTP07498023.1	529	2506.K20.GZ43_366817
23437	DTT07600010.1	1528	DTP07600019.1	902	2464.H17.GZ43_357865
23438	DTT08005024.1	1529	DTP08005033.1	1046	2475.N21.GZ43_362334
23439	DTT08098020.1	1530	DTP08098029.1	485	2540.M18.GZ43_372313
23440	DTT08167018.1	1531	DTP08167027.1	152	2365.N12.GZ43_345550
23440	DTT08167018.1	1531	DTP08167027.1	544	2542.F05.GZ43_372900
23441	DTT08249022.1	1532	DTP08249031.1	1235	2498.G15.GZ43_365010
23442	DTT08499022.1	1533	DTP08499031.1	452	2540.A24.GZ43_372031
23443	DTT08514022.1	1534	DTP08514031.1	508	2541.L12.GZ43_372667

23444	DTT08527013.1	1535	DTP08527022.1	109	2510.N14.GZ43_369351
23444	DTT08527013.1	1535	DTP08527022.1	394	2554.A16.GZ43_375863
23444	DTT08527013.1	1535	DTP08527022.1	1128	2489.F09.GZ43_362957
23444	DTT08527013.1	1535	DTP08527022.1	569	2555.F16.GZ43_373295
23445	DTT08595020.1	1536	DTP08595029.1	413	2554.N09.GZ43_376168
23446	DTT08711019.1	1537	DTP08711028.1	472	2540.C19.GZ43_372074
23447	DTT08773020.1	1538	DTP08773029.1	687	2559.I12.GZ43_374899
23448	DTT08874012.1	1539	DTP08874021.1	356	2537.P14.GZ43_371229
23449	DTT09387018.1	1540	DTP09387027.1	762	2561.P19.GZ43_376610
23450	DTT09396022.1	1541	DTP09396031.1	1140	2489.M11.GZ43_363127
23451	DTT09553027.1	1542	DTP09553036.1	54	2505.J22.GZ43_366411
23452	DTT09604016.1	1543	DTP09604025.1	1100	2483.J07.GZ43_359878
23453	DTT09705033.1	1544	DTP09705042.1	323	2536.O22.GZ43_370829
23454	DTT09742009.1	1545	DTP09742018.1	766	2456.B12.GZ43_355864
23454	DTT09742009.1	1545	DTP09742018.1	563	2542.N21.GZ43_373108
23455	DTT09753017.1	1546	DTP09753026.1	910	2464.L02.GZ43_357946
23456	DTT09793019.1	1547	DTP09793028.1	904	2464.I04.GZ43_357876
23457	DTT09796028.1	1548	DTP09796037.1	189	2366.L21.GZ43_345942
23458	DTT10221016.1	1549	DTP10221025.1	592	2556.C19.GZ43_373610
23459	DTT10360040.1	1550	DTP10360049.1	1045	2475.M20.GZ43_362309
23460	DTT10539016.1	1551	DTP10539025.1	527	2506.J20.GZ43_366793
23461	DTT10564022.1	1552	DTP10564031.1	1035	2475.H06.GZ43_362175
23462	DTT10683041.1	1553	DTP10683050.1	561	2542.K21.GZ43_373036
23463	DTT10819011.1	1554	DTP10819020.1	796	2457.C19.GZ43_356279
23463	DTT10819011.1	1554	DTP10819020.1	143	2365.J14.GZ43_345456
23463	DTT10819011.1	1554	DTP10819020.1	1023	2474.I06.GZ43_361815
23464	DTT11363027.1	1555	DTP11363036.1	540	2542.C20.GZ43_372843
23465	DTT11479018.1	1556	DTP11479027.1	521	2506.G24.GZ43_366725
23466	DTT11483012.1	1557	DTP11483021.1	877	2459.H09.GZ43_357169
23467	DTT11548015.1	1558	DTP11548024.1	422	2565.C17.GZ43_398204
23468	DTT11730017.1	1559	DTP11730026.1	264	2535.B09.GZ43_370120
23469	DTT11791010.1	1560	DTP11791019.1	518	2506.E12.GZ43_366665
23470	DTT11864036.1	1561	DTP11864045.1	778	2456.H07.GZ43_356003
23471	DTT11902028.1	1562	DTP11902037.1	1144	2490.B06.GZ43_363242
23472	DTT11915017.1	1563	DTP11915026.1	591	2556.C11.GZ43_373602

23472	DTT11915017.1	1563	DTP11915026.1	1021	2474.G17.GZ43_361778
23472	DTT11915017.1	1563	DTP11915026.1	1163	2491.C13.GZ43_363657
23473	DTT11966040.1	1564	DTP11966049.1	1216	2562.E14.GZ43_375573
23473	DTT11966040.1	1564	DTP11966049.1	818	2457.L21.GZ43_356497
23473	DTT11966040.1	1564	DTP11966049.1	532	2506.M13.GZ43_366858
23474	DTT12042027.1	1565	DTP12042036.1	874	2459.G01.GZ43_357137
23475	DTT12201062.1	1566	DTP12201071.1	759	2561.O17.GZ43_376584
23475	DTT12201062.1	1566	DTP12201071.1	1207	2562.B09.GZ43_375496
23476	DTT12470020.1	1567	DTP12470029.1	1124	2489.A13.GZ43_362841
23476	DTT12470020.1	1567	DTP12470029.1	799	2457.D12.GZ43_356296
23476	DTT12470020.1	1567	DTP12470029.1	690	2559.J02.GZ43_374913
23476	DTT12470020.1	1567	DTP12470029.1	568	2555.E20.GZ43_373275
23477	DTT12550009.1	1568	DTP12550018.1	12	2504.G01.GZ43_365934

Table 148

SEQ ID	SEQ NAME	ACCES- SION	GENBANK DESCRIPTION	GENBA NK SCORE
22006	2504.C08.GZ4 3_365845	AP000321	gi 4835690 dbj AP000321.1AP000321 Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:Q82F5, complete sequence	1.6E-31
22007	2504.C11.GZ4 3_365848	AP002938	gi 16267134 dbj AP002938.1AP002938 Hoplostethus japonicus mitochondrial DNA, complete genome	4.8E-58
22009	2504.D16.GZ4 3_365877	AK023496	gi 10435445 dbj AK023496.1AK023496 Homo sapiens cDNA FLJ13434 fis, clone PLACE1002578	0
22010	2504.E23.GZ4 3_365908	M80340	gi 339767 gb M80340.1HUMTNL12 Human transposon L1.1 with a base deletion relative to L1.2B resulting in a premature stop codon in t	6.1E-182
22011	2504.F20.GZ4 3_365929	AE007289	gi 14524175 gb AE007289.1AE007289 Sinorhizobium meliloti plasmid pSymA section 95 of 121 of the complete plasmid sequence	2.1E-98

22017	2504.I13.GZ4 3_365994	AJ312523	gi 12830519 emb AJ312523.1GGO312523 Gorilla gorilla gorilla Xq13.3 chromosome non-coding sequence, isolate G167W	1.1E-44
22031	2504.O12.GZ4 3_366137	AF342020	gi 12961941 gb AF342020.1AF342020 Sclerotinia sclerotiorum strain LES-1 28S ribosomal RNA gene, partial sequence; intergenic spacer	1.1E-90
22033	2505.B05.GZ4 3_366202	U93571	gi 2072968 gb U93571.1HSU93571 Human L1 element L1.24 p40 gene, complete cds	1.1E-226
22037	2505.C17.GZ4 3_366238	AJ325713	gi 15870107 emb AJ325713.1HSA325713 Homo sapiens genomic sequence surrounding NotI site, clone NB1-110S	1.4E-21
22040	2505.D03.GZ4 3_366248	AJ224335	gi 3413799 emb AJ224335.1HSAJ4335 Homo sapien mRNA for putative secretory protein, hBET3	5.2E-71
22043	2505.E15.GZ4 3_366284	AB030001	gi 7416074 dbj AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	8.1E-55
22046	2505.G16.GZ4 3_366333	AE005683	gi 13421186 gb AE005683.1AE005683 Caulobacter crescentus section 9 of 359 of the complete genome	3.6E-63
22048	2505.I04.GZ4 3_366369	AF255613	gi 8925326 gb AF255613.1AF255613 Homo sapiens teratoma-associated tyrosine kinase (TAPK) gene, exons 1 through 6 and partial cds	7.9E-73
22063	2505.O09.GZ4 3_366518	AF053644	gi 3598786 gb AF053644.1HSCSE1G2 Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exon 2	9.4E-45
22072	2510.C10.GZ4 3_369083	AB002353	gi 2224650 dbj AB002353.1AB002353 Human mRNA for KIAA0355 gene, complete cds	1.4E-71
22078	2510.G06.GZ4 3_369175	AF084935	gi 3603422 gb AF084935.1AF084935 Homo sapiens galactokinase (GALK1) gene, partial cds	8.9E-24

22089	2510.J11.GZ4 3_369252	AK024617	gi 10436933 dbj AK024617.1AK024617 Homo sapiens cDNA: FLJ20964 fis, clone ADSH00902	0
22102	2510.L21.GZ4 3_369310	AK023677	gi 10435673 dbj AK023677.1AK023677 Homo sapiens cDNA FLJ13615 fis, clone PLACE1010896, weakly similar to NUF1 PROTEIN	1.2E-90
22109	2510.N14.GZ4 3_369351	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
22115	2510.O23.GZ4 3_369384	AF113169	gi 4164598 gb AF113169.1AF113169 Homo sapiens glandular kallikrein enhancer region, complete sequence	2.2E-39
22124	2365.C20.GZ4 3_345294	AF069489	gi 3560568 gb AF069489.1HSPDE4A3 Homo sapiens cAMP specific phosphodiesterase 4A variant pde46 (PDE4A) gene, exons 2 through 13 and	6.6E-24
22134	2365.F24.GZ4 3_345370	AK012908	gi 12849956 dbj AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	2.9E-224
22143	2365.J14.GZ4 3_345456	BC007999	gi 14124949 gb BC007999.1BC007999 Homo sapiens, hypothetical protein FLJ10759, clone MGC:15757 IMAGE:3357436, mRNA, complete cds	4.4E-56
22152	2365.N12.GZ4 3_345550	U20391	gi 1483626 gb U20391.1HSU20391 Human folate receptor (FOLR1) gene, complete cds	3.9E-41
22162	2366.E03.GZ4 3_345647	AB025285	gi 5917586 dbj AB025285.1AB025285 Homo sapiens c-ERBB-2 gene, exons 1', 2', 3', 4'	4.3E-30
22163	2366.J03.GZ4 3_345652	M15885	gi 338414 gb M15885.1HUMSPP Human prostate secreted seminal plasma protein mRNA, complete cds	1.1E-68
22170	2366.J06.GZ4 3_345700	AF326517	gi 15080738 gb AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	0

22182	2366.K13.GZ4 3_345813	U27333	gi 967202 gb U27333.1HSU27333 Human alpha (1,3) fucosyltransferase (FUT6) mRNA, major transcript I, complete cds	2.5E-44
22189	2366.L21.GZ4 3_345942	AF272390	gi 8705239 gb AF272390.1AF272390 Homo sapiens myosin 5c (MYO5C) mRNA, complete cds	1.4E-290
22195	2367.B10.GZ4 3_346028	AJ279823	gi 11932035 emb AJ279823.1ASF279823 Ascovirus SfAV1b partial pol gene for DNA polymerase, Pol2-Pol3-Pol1 fragment	1.4E-231
22198	2367.C12.GZ4 3_346054	BC014669	gi 15779227 gb BC014669.1BC014669 Homo sapiens, clone IMAGE:4849317, mRNA, partial cds	2.9E-57
22200	2367.D18.GZ4 3_346084	AE008517	gi 15459138 gb AE008517.1AE008517 Streptococcus pneumoniae R6 section 133 of 184 of the complete genome	1.4E-34
22205	2367.F06.GZ4 3_346120	AJ330464	gi 15874882 emb AJ330464.1HSA330464 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IL7C	3.1E-100
22206	2367.F13.GZ4 3_346127	AY035075	gi 14334803 gb AY035075.1 Arabidopsis thaliana putative H ⁺ -transporting ATPase (AT4g30190) mRNA, complete cds	4.1E-229
22208	2367.G13.GZ4 3_346151	AK025355	gi 10437854 dbj AK025355.1AK025355 Homo sapiens cDNA: FLJ21702 fis, clone COL09874	1.8E-58
22209	2367.G17.GZ4 3_346155	AK000293	gi 7020278 dbj AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	4.4E-34
22210	2367.G20.GZ4 3_346158	AL137592	gi 6808332 emb AL137592.1HSM802347 Homo sapiens mRNA; cDNA DKFZp434L0610 (from clone DKFZp434L0610); partial cds	1.6E-60
22211	2367.G22.GZ4 3_346160	BC015529	gi 15930193 gb BC015529.1BC015529 Homo sapiens, Similar to ribose 5- phosphate isomerase A, clone MGC:9441 IMAGE:3904718, mRNA, comp	9.7E-60

22213	2367.I15.GZ4 3_346201	AF324172	gi 12958747 gb AF324172.1AF324172 Dictyophora indusiata strain ASI 32001 internal transcribed spacer 1, partial sequence; 5.8S ribo	4.8E-65
22217	2367.K24.GZ4 3_346258	AF009251	gi 2352833 gb AF009251.1CLCN6HUM0 5 Homo sapiens putative chloride channel gene (CLCN6), exon 6	3.8E-62
22219	2367.M06.GZ 43_346288	AF178322	gi 13344845 gb AF178322.1AF178322 Schmidtea mediterranea cytochrome oxidase C subunit I (COI) gene, partial cds; mitochondrial gene	1.5E-43
22220	2367.M14.GZ 43_346296	AK026286	gi 10439097 dbj AK026286.1AK026286 Homo sapiens cDNA: FLJ22633 fis, clone HSI06502	1E-300
22221	2367.M16.GZ 43_346298	AF368920	gi 14039926 gb AF368920.1AF368920 Caenorhabditis elegans voltage-dependent calcium channel alpha13 subunit (cca-1) mRNA, complete c	1.6E-83
22224	2367.N16.GZ4 3_346322	Z78727	gi 1508005 emb Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.3E-37
22231	2368.B18.GZ4 3_346420	AK000293	gi 7020278 dbj AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	5E-34
22235	2368.D08.GZ4 3_346458	AJ276936	gi 12214232 emb AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
22245	2368.I04.GZ4 3_346574	AY042191	gi 15546022 gb AY042191.1 Mus musculus RF-amide G protein-coupled receptor (MrgA1) mRNA, complete cds	3.1E-26
22249	2368.K21.GZ4 3_346639	AJ310931	gi 15718363 emb AJ310931.1HSA310931 Homo sapiens mRNA for myosin heavy chain	7E-55
22252	2368.M19.GZ 43_346685	AK025595	gi 10438161 dbj AK025595.1AK025595 Homo sapiens cDNA: FLJ21942 fis, clone HEP04527	4.7E-21

22257	2368.N15.GZ4 3_346705	AK014328	gi 12852104 dbj AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	3.1E-103
22258	2368.N23.GZ4 3_346713	AL391428	gi 9864373 emb AL391428.1AL391428 Human DNA sequence from clone RP11- 60P19 on chromosome 1, complete sequence [Homo sapiens]	4.8E-28
22259	2368.O03.GZ4 3_346717	AK012908	gi 12849956 dbj AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	2.1E-227
22260	2368.O11.GZ4 3_346725	AF102129	gi 5922722 gb AF102129.1AF102129 Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds	2.5E-103
22264	2535.B09.GZ4 3_370120	AF292648	gi 12656358 gb AF292648.1AF292648 Mus-musculus zinc finger 202 m1 (Znf202) mRNA, complete cds	2E-39
22267	2535.C23.GZ4 3_370158	AF307053	gi 12018057 gb AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
22269	2535.F05.GZ4 3_370212	AF367433	gi 14486704 gb AF367433.1AF367433 Lotus japonicus phosphatidylinositol transfer-like protein III (LjPLP-III) mRNA, complete cds	3.8E-38
22276	2535.L03.GZ4 3_370354	AK000099	gi 7019966 dbj AK000099.1AK000099 Homo sapiens cDNA FLJ20092 fis, clone COL04215	7.1E-52
22280	2535.O07.GZ4 3_370430	BC008425	gi 14250051 gb BC008425.1BC008425 Homo sapiens, clone MGC:14582 IMAGE:4246114, mRNA, complete cds	3.8E-34
22282	2535.P02.GZ4 3_370449	NM_024074	gi 13129059 ref NM_024074.1 Homo sapiens hypothetical protein MGC3169 (MGC3169), mRNA	2.4E-23

22292	2536.A22.GZ4 3_370493	AF310311	gi 13517433 gb AF310311.1AF310311 Homo sapiens isolate Nigeria 9 membrane protein CH1 gene, partial cds	0
22297	2536.D17.GZ4 3_370560	AF015148	gi 2353128 gb AF015148.1AF015148 Homo sapiens clone HS19.2 Alu-Ya5 sequence	1.6E-46
22303	2536.G05.GZ4 3_370620	AF045605	gi 3228525 gb AF045605.1AF045605 Homo sapiens germline chromosome 11, 11q13 region	6.2E-77
22305	2536.G21.GZ4 3_370636	AK026490	gi 10439363 dbj AK026490.1AK026490 Homo sapiens cDNA: FLJ22837 fis, clone KAIA4417	3.5E-143
22306	2536.G22.GZ4 3_370637	NC_002707	gi 13540758 ref NC_002707.1 Anguilla japonica mitochondrion, complete genome	2.3E-39
22309	2536.I05.GZ4 3_370668	AK000099	gi 7019966 dbj AK000099.1AK000099 Homo sapiens cDNA FLJ20092 fis, clone COL04215	3.4E-63
22310	2536.I15.GZ4 3_370678	AB013897	gi 6177784 dbj AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	5.1E-53
22313	2536.J11.GZ4 3_370698	AK023448	gi 10435386 dbj AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
22314	2536.K12.GZ4 3_370723	U14573	gi 551542 gb U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1E-96
22319	2536.N05.GZ4 3_370788	AK001347	gi 7022548 dbj AK001347.1AK001347 Homo sapiens cDNA FLJ10485 fis, clone NT2RP2000195	6.7E-43
22320	2536.N20.GZ4 3_370803	Y15724	gi 3021395 emb Y15724.1HSSERCA1 Homo sapiens SERCA3 gene, exons 1-7 (and joined CDS)	1.9E-27
22330	2537.B07.GZ4 3_370886	X69516	gi 288876 emb X69516.1HSFOLA H.sapiens gene for folate receptor	2.8E-60

22334	2537.D11.GZ4 3_370938	NM_025080	gi 13376633 ref NM_025080.1 Homo sapiens hypothetical protein FLJ22316 (FLJ22316), mRNA	8.7E-289
22338	2537.G05.GZ4 3_371004	L04193	gi 187144 gb L04193.1HUMLMGP Human lens membrane protein (mp19) gene, exon 11	7.4E-52
22341	2537.I03.GZ4 3_371050	Z78727	gi 1508005 emb Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.7E-37
22345	2537.K17.GZ4 3_371112	AL603947	gi 15384818 emb AL603947.1UMA0006 Ustilago maydis gene for predicted plasmamembrane-ATPase	9.3E-76
22350	2537.N23.GZ4 3_371190	AF242865	gi 9858570 gb AF242865.1AF242862S4 Homo sapiens coxsackie virus and adenovirus receptor (CXADR) gene, exon 7 and complete cds	2.4E-30
22352	2537.O05.GZ4 3_371196	AB060827	gi 13874462 dbj AB060827.1AB060827 Macaca fascicularis brain cDNA clone:QtrA-10256, full insert sequence	2.2E-24
22356	2537.P14.GZ4 3_371229	AK026442	gi 10439307 dbj AK026442.1AK026442 Homo sapiens cDNA: FLJ22789 fis, clone KAIA2171	6.3E-256
22361	2538.A10.GZ4 3_371249	AK001432	gi 7022685 dbj AK001432.1AK001432 Homo sapiens cDNA FLJ10570 fis, clone NT2RP2003117	1.9E-52
22363	2538.B03.GZ4 3_371266	AK013900	gi 12851449 dbj AK013900.1AK013900 Mus musculus 12 days embryo head cDNA, RIKEN full-length enriched library, clone:3010026L22, ful	1.2E-201
22366	2538.C07.GZ4 3_371294	AK022973	gi 10434673 dbj AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	0
22367	2538.C14.GZ4 3_371301	M87914	gi 174891 gb M87914.1HUMALNE461 Human carcinoma cell-derived Alu RNA transcript, clone NE461	2E-89

22368	2538.D03.GZ4 3_371314	AK022973	gi 10434673 dbj AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	4.3E-275
22369	2538.D04.GZ4 3_371315	AK022973	gi 10434673 dbj AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	1.3E-287
22371	2538.E01.GZ4 3_371336	AF074397	gi 3916231 gb AF074397.1AF074397 Homo sapiens anti-mullerian hormone type II receptor (AMHR2) gene, promoter region and partial cds	4E-40
22374	2538.F03.GZ4 3_371362	L34639	gi 598203 gb L34639.1HUMPECAM09 Homo sapiens platelet/endothelial cell adhesion molecule-1 (PECAM-1) gene, exon 6	1.5E-43
22375	2538.H02.GZ4 3_371409	AF220173	gi 9651700 gb AF220173.1AF220172S2 Homo sapiens acid ceramidase (ASAH) gene, exons 2 through 4	2.5E-39
22379	2538.I17.GZ4 3_371448	AF050179	gi 3319283 gb AF050179.1AF050179 Homo sapiens CENP-C binding protein (DAXX) mRNA, complete cds	4.9E-41
22380	2538.J10.GZ4 3_371465	AY035075	gi 14334803 gb AY035075.1 Arabidopsis thaliana putative H ⁺ -transporting ATPase (AT4g30190) mRNA, complete cds	3.5E-245
22381	2538.K17.GZ4 3_371496	AK022749	gi 10434332 dbj AK022749.1AK022749 Homo sapiens cDNA FLJ12687 fis, clone NT2RM4002532, weakly similar to PROTEIN HOM1	1.5E-31
22385	2538.M16.GZ 43_371543	AF375410	gi 14030638 gb AF375410.1AF375410 Arabidopsis thaliana At2g43970/F6E13.10 gene, complete cds	1.9E-53
22386	2538.M17.GZ 43_371544	AK025473	gi 10437996 dbj AK025473.1AK025473 Homo sapiens cDNA: FLJ21820 fis, clone HEP01232	3.2E-282

22389	2538.P16.GZ4 3_371615	AK026286	gi 10439097 dbj AK026286.1AK026286 Homo sapiens cDNA: FLJ22633 fis, clone HSI06502	0
22391	2554.A06.GZ4 3_375853	AK001324	gi 7022509 dbj AK001324.1AK001324 Homo sapiens cDNA FLJ10462 fis, clone NT2RP1001494, weakly similar to MALE STERILITY PROTEIN 2	4E-44
22394	2554.A16.GZ4 3_375863	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
22406	2554.I15.GZ4 3_376054	AY050376	gi 15215695 gb AY050376.1 Arabidopsis thaliana AT3g16950/K14A17_7 mRNA, complete cds	8.8E-27
22415	2554.P16.GZ4 3_376223	AK022368	gi 10433751 dbj AK022368.1AK022368 Homo sapiens cDNA FLJ12306 fis, clone MAMMA1001907	6.7E-46
22418	2565.B13.GZ4 3_398139	AL050012	gi 4884261 emb AL050012.1HSM800354 Homo sapiens mRNA; cDNA DKFZp564K133 (from clone DKFZp564K133)	1E-44
22419	2565.B15.GZ4 3_398171	AY049285	gi 15146287 gb AY049285.1 Arabidopsis thaliana AT3g58570/F14P22_160 mRNA, complete cds	2.1E-62
22422	2565.C17.GZ4 3_398204	M24543	gi 341200 gb M24543.1HUMPSANTIG Human prostate-specific antigen (PA) gene, complete cds	2.5E-49
22423	2565.D06.GZ4 3_398029	AF331321	gi 13095271 gb AF331321.1AF331321 HIV1 isolate T7C44 from the Netherlands nonfunctional pol polyprotein gene, partial sequence	4.7E-30
22428	2565.G20.GZ4 3_398256	AJ276936	gi 12214232 emb AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
22429	2565.H01.GZ4 3_397953	AF326517	gi 15080738 gb AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	1E-300

22433	2565.I22.GZ4 3_398290	AK001926	gi 7023492 dbj AK001926.1AK001926 Homo sapiens cDNA FLJ11064 fis, clone PLACE1004824	8.9E-295
22442	2565.M14.GZ4 43_398166	AF275699	gi 12275949 gb AF275699.1AF275699 Unidentified Hailaer soda lake bacterium F16 16S ribosomal RNA gene, partial sequence	1.4E-21
22447	2565.O07.GZ4 3_398056	AK024752	gi 10437118 dbj AK024752.1AK024752 Homo sapiens cDNA: FLJ21099 fis, clone CAS04610	4.3E-51
22452	2540.A24.GZ4 3_372031	Z69920	gi 1217632 emb Z69920.1HS91K3D Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3	1.1E-41
22463	2540.H07.GZ4 3_372182	AE008025	gi 15155943 gb AE008025.1AE008025 Agrobacterium tumefaciens strain C58 circular chromosome, section 83 of 254 of the complete seque	1.7E-40
22465	2540.I10.GZ4 3_372209	AK000658	gi 7020892 dbj AK000658.1AK000658 Homo sapiens cDNA FLJ20651 fis, clone KAT01814	1.3E-53
22468	2540.M22.GZ4 43_372317	AF375597	gi 14150816 gb AF375597.1AF375596S2 Mus musculus medium and short chain L-3- hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exo	0
22472	2540.C19.GZ4 3_372074	AB019559	gi 4579750 dbj AB019559.1AB019559 Sus scrofa mRNA for 130 kDa regulatory subunit of myosin phosphatase, partial cds	3.1E-24
22477	2540.F15.GZ4 3_372142	AY016428	gi 13891961 gb AY016428.1 Plasmodium falciparum isolate Fas 30-6-7 apical membrane antigen-1 (AMA-1) gene, partial cds	2.2E-33
22485	2540.M18.GZ4 43_372313	AJ331177	gi 15875595 emb AJ331177.1HSA331177 Homo sapiens genomic sequence surrounding NotI site, clone NL1-ZF18RS	7.7E-237

22507	2541.L08.GZ4 3_372663	BC003673	gi 13277537 gb BC003673.1BC003673 Homo sapiens, protamine 1, clone MGC:12307 IMAGE:3935638, mRNA, complete cds	2.6E-53
22508	2541.L12.GZ4 3_372667	AJ297708	gi 12055486 emb AJ297708.1RNO297708 Rattus norvegicus RT6 gene for T cell differentiation marker RT6.2, exons 1-8	9.4E-45
22514	2506.C15.GZ4 3_366620	AE007488	gi 14973493 gb AE007488.1AE007488 Streptococcus pneumoniae TIGR4 section 171 of 194 of the complete genome	1.4E-287
22519	2506.E18.GZ4 3_366671	AK025164	gi 10437625 dbj AK025164.1AK025164 Homo sapiens cDNA: FLJ21511 fis, clone. COL05748	0
22521	2506.G24.GZ4 3_366725	AY030962	gi 13736961 gb AY030962.1 HIV-1 isolate NC3964-1999 from USA pol polypeptide (pol) gene, partial cds	9.1E-233
22527	2506.J20.GZ4 3_366793	AF152924	gi 5453323 gb AF152924.1AF152924 Mus musculus syntaxin4-interacting protein synip mRNA, complete cds	2.3E-79
22528	2506.J22.GZ4 3_366795	AK000169	gi 7020080 dbj AK000169.1AK000169 Homo sapiens cDNA FLJ20162 fis, clone COL09280	1.8E-99
22531	2506.M05.GZ 43_366850	AE007580	gi 15023517 gb AE007580.1AE007580 Clostridium acetobutylicum ATCC824 section 68 of 356 of the complete genome	2.1E-217
22534	2506.P07.GZ4 3_366924	AF035442	gi 3142369 gb AF035442.1AF035442 Homo sapiens VAV-like protein mRNA, partial cds	1E-44
22540	2542.C20.GZ4 3_372843	AE007424	gi 14972724 gb AE007424.1AE007424 Streptococcus pneumoniae TIGR4 section 107 of 194 of the complete genome	2.3E-42
22543	2542.D19.GZ4 3_372866	BC008333	gi 14249906 gb BC008333.1BC008333 Homo sapiens, clone IMAGE:3506145, mRNA, partial cds	5.3E-284

22544	2542.F05.GZ4 3_372900	AK024179	gi 10436495 dbj AK024179.1AK024179 Homo sapiens cDNA FLJ14117 fis, clone MAMMA1001785	2.4E-41
22553	2542.M09.GZ4 43_373072	AK022973	gi 10434673 dbj AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	5.8E-243
22557	2542.P19.GZ4 3_373154	AK025164	gi 10437625 dbj AK025164.1AK025164 Homo sapiens cDNA: FLJ21511 fis, clone COL05748	0
22562	2542.M24.GZ4 43_373087	AK022173	gi 10433509 dbj AK022173.1AK022173 Homo sapiens cDNA FLJ12111 fis, clone MAMMA1000025	1.2E-284
22563	2542.N21.GZ4 3_373108	AF025409	gi 2582414 gb AF025409.1AF025409 Homo sapiens zinc transporter 4 (ZNT4) mRNA, complete cds	2E-70
22567	2555.D22.GZ4 3_373253	AL157697	gi 11121002 emb AL157697.1AL157697 Human DNA sequence from clone RP5- 1092C14 on chromosome 6, complete sequence [Homo sapiens]	1.1E-87
22568	2555.E20.GZ4 3_373275	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
22569	2555.F16.GZ4 3_373295	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
22574	2555.K17.GZ4 3_373416	AK026686	gi 10439593 dbj AK026686.1AK026686 Homo sapiens cDNA: FLJ23033 fis, clone LNG02005	1.8E-23
22578	2555.P22.GZ4 3_373541	AF087913	gi 5081331 gb AF087913.1AF087913 Human endogenous retrovirus HERV-P- T47D	5.8E-74
22579	2555.A11.GZ4 3_373170	NC_000957	gi 11497445 ref NC_000957.1 Borrelia burgdorferi plasmid lp5, complete sequence	1.3E-57

22585	2555.I12.GZ4 3_373363	AJ276936	gi 12214232 emb AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	1.6E-237
22589	2556.A02.GZ4 3_373545	AE007289	gi 14524175 gb AE007289.1AE007289 Sinorhizobium meliloti plasmid pSymA section 95 of 121 of the complete plasmid sequence	2E-55
22591	2556.C11.GZ4 3_373602	AY039252	gi 15418981 gb AY039252.1 Macaca mulatta immunoglobulin alpha heavy chain constant region (IgA) gene, IgA-C.II allele, partial cds	3.1E-29
22602	2556.H15.GZ4 3_373726	AK021966	gi 10433275 dbj AK021966.1AK021966 Homo sapiens cDNA FLJ11904 fis, clone HEMBB1000048	1.6E-70
22620	2557.B22.GZ4 3_373973	AB071392	gi 15721873 dbj AB071392.1AB071392 Expression vector pAQ-EX1 DNA, complete sequence	1.2E-25
22627	2557.J14.GZ4 3_374157	AK023721	gi 10435737 dbj AK023721.1AK023721 Homo sapiens cDNA FLJ13659 fis, clone PLACE1011576, moderately similar to Human Kruppel related	1.6E-209
22635	2557.N14.GZ4 3_374253	AB013897	gi 6177784 dbj AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	1E-44
22648	2558.B24.GZ4 3_374359	AB064318	gi 14595115 dbj AB064318.1AB064318 Comamonas testosteroni gene for 16S rRNA, partial sequence	4.6E-28
22657	2558.G07.GZ4 3_374462	M92069	gi 337698 gb M92069.1HUMRTVLC Human retrovirus-like sequence-isoleucine c (RTVL-Ic) gene, Alu repeats	6.7E-46
22661	2558.H17.GZ4 3_374496	AK023812	gi 10435860 dbj AK023812.1AK023812 Homo sapiens cDNA FLJ13750 fis, clone PLACE3000331	5.2E-31

22662	2558.J01.GZ4 3_374528	AK023448	gi 10435386 dbj AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	4.8E-278
22666	2558.K02.GZ4 3_374553	U14573	gi 551542 gb U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1.3E-62
22683	2559.D05.GZ4 3_374772	AF338713	gi 14039582 gb AF338713.1AF338713 Casuarius casuarius mitochondrion, partial genome	4E-297
22687	2559.I12.GZ4 3_374899	AY036096	gi 14486435 gb AY036096.1 HIV-1 isolate L2Q2P from Belgium reverse transcriptase (pol) gene, partial cds	1.4E-41
22690	2559.J02.GZ4 3_374913	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
22692	2559.K12.GZ4 3_374947	Z96776	gi 2181853 emb Z96776.1HS9QT023 H.sapiens telomeric DNA sequence, clone 9QTEL023, read 9QTELOO023.seq	5.1E-52
22694	2559.L09.GZ4 3_374968	AE007426	gi 14972746 gb AE007426.1AE007426 Streptococcus pneumoniae TIGR4 section 109 of 194 of the complete genome	8.1E-21
22696	2559.M21.GZ 43_375004	AJ414564	gi 15990852 emb AJ414564.1HSA414564 Homo sapiens mRNA for connexin40.1 (CX40.1 gene)	9.2E-30
22698	2559.N13.GZ4 3_375020	AL137330	gi 6807822 emb AL137330.1HSM802010 Homo sapiens mRNA; cDNA DKFZp434F0272 (from clone DKFZp434F0272)	4.1E-47
22714	2560.H01.GZ4 3_375248	U14567	gi 551536 gb U14567.1HSU14567 ***ALU WARNING: Human Alu-J subfamily consensus sequence	2.7E-42
22719	2560.K02.GZ4 3_375321	AF178754.3	gi 7770069 gb AF178754.3AF178754 Homo sapiens lithium-sensitive myo- inositol monophosphatase A1 (IMPA1) gene, promoter region and p	3.1E-51

22720	2560.K08.GZ4 3_375327	AK009327	gi 12844057 dbj AK009327.1AK009327 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310012P17, full	6.3E-80
22721	2560.K10.GZ4 3_375329	AF344987	gi 13448249 gb AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	1E-300
22729	2560.O08.GZ4 3_375423	AY037285	gi 15982643 gb AY037285.1AY037284S2 HIV-1 from Cameroon vpu protein (vpu) and envelope glycoprotein (env) genes, complete cds; and	5.2E-54
22732	2561.B03.GZ4 3_376258	AF035968.2	gi 8714504 gb AF035968.2AF035968 Homo sapiens integrin alpha 2 (ITGA2) gene, ITGA2-1 allele, exons 6-9, and partial cds	3.9E-32
22733	2561.B12.GZ4 3_376267	AP000276	gi 4835645 dbj AP000276.1AP000276 Homo sapiens genomic DNA, chromosome 21q22.1, D21S226-AML region, clone:55A9, complete sequence	1.9E-27
22750	2561.M09.GZ 43_376528	AF052684	gi 2995716 gb AF052684.1HSPRCAD2 Homo sapiens protocadherin 43 gene, exon 2	4.1E-41
22753	2561.E22.GZ4 3_376349	AF132952	gi 4680674 gb AF132952.1AF132952 Homo sapiens CGI-18 protein mRNA, complete cds	3E-41
22754	2561.G20.GZ4 3_376395	U14573	gi 551542 gb U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	1.5E-71
22755	2561.H17.GZ4 3_376416	AF052685	gi 2995717 gb AF052685.1HSPRCAD3 Homo sapiens protocadherin 43 gene, exon 3, exon 4, and complete cds	2.1E-24
22756	2561.I19.GZ4 3_376442	AF344987	gi 13448249 gb AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	3.2E-201
22761	2561.P16.GZ4 3_376607	Z78727	gi 1508005 emb Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.6E-37

22762	2561.P19.GZ4 3_376610	U66535	gi 2270915 gb U66535.1HSITGBF07 Human beta4-integrin (ITGB4) gene, exons 19,20,21,22,23,24 and 25	8.6E-41
22763	2561.P23.GZ4 3_376614	AF167458	gi 6467463 gb AF167458.1HSDSRPKR04 Homo sapiens double stranded RNA activated protein kinase (PKR) gene, intron 1	1E-22
22771	2456.D04.GZ4 3_355904	AF307053	gi 12018057 gb AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
22777	2456.H02.GZ4 3_355998	AJ005821	gi 3123571 emb AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	5.8E-37
22788	2456.N23.GZ4 3_356163	AF188746	gi 6425045 gb AF188746.1AF188746 Homo sapiens prostrate kallikrein 2 (KLK2) mRNA, complete cds	9.6E-63
22796	2457.C19.GZ4 3_356279	AF368920	gi 14039926 gb AF368920.1AF368920 Caenorhabditis elegans voltage-dependent calcium channel alpha13 subunit (cca-1) mRNA, complete c	1E-47
22799	2457.D12.GZ4 3_356296	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0
22810	2457.H17.GZ4 3_356397	AE007614	gi 15023883 gb AE007614.1AE007614 Clostridium acetobutylicum ATCC824 section 102 of 356 of the complete genome	9E-63
22823	2458.A10.GZ4 3_356618	AK026920	gi 10439892 dbj AK026920.1AK026920 Homo sapiens cDNA: FLJ23267 fis, clone COL07266	6.2E-84
22827	2458.B23.GZ4 3_356655	AB050432	gi 10998295 dbj AB050432.1AB050432 Macaca fascicularis brain cDNA, clone:QnpA-21861	4.3E-129
22829	2458.C06.GZ4 3_356662	U49973	gi 2226003 gb U49973.1HSU49973 Human Tigger1 transposable element, complete consensus sequence	2E-24

22842	2458.I09.GZ4 3_356809	AK023496	gi 10435445 dbj AK023496.1AK023496 Homo sapiens cDNA FLJ13434 fis, clone PLACE1002578	2.4E-39
22843	2458.I10.GZ4 3_356810	AF031077	gi 6649934 gb AF031077.1AF031077 Homo sapiens chromosome X, cosmid LLNLc110C1837, complete sequence	1.3E-52
22845	2458.I17.GZ4 3_356817	AK026569	gi 10439451 dbj AK026569.1AK026569 Homo sapiens cDNA: FLJ22916 fis, clone KAT06406, highly similar to HSCYCR Human mRNA for T-cell	1.8E-38
22846	2458.I20.GZ4 3_356820	AF184614	gi 6983939 gb AF184614.1AF184614 Homo sapiens p47-phox (NCF1) gene, complete cds	4.2E-33
22855	2458.N06.GZ4 3_356926	AF367251	gi 14161363 gb AF367251.1AF367251 Helicobacter pylori strain CAPM N93 cytotoxin associated protein A (cagA) gene, complete cds	2.2E-70
22865	2459.B11.GZ4 3_357027	AF375597	gi 14150816 gb AF375597.1AF375596S2 Mus musculus medium and short chain L-3- hydroxyacyl-Coenzyme A dehydrogenase (Mschad) gene, exo	0
22866	2459.C05.GZ4 3_357045	X04803.2	gi 6647297 emb X04803.2HSYUBG1 Homo sapiens ubiquitin gene	6.4E-52
22873	2459.F20.GZ4 3_357132	AK025207	gi 10437672 dbj AK025207.1AK025207 Homo sapiens cDNA: FLJ21554 fis, clone COL06330	0
22877	2459.H09.GZ4 3_357169	AB046623	gi 9651056 dbj AB046623.1AB046623 Macaca fascicularis brain cDNA, clone QccE-10576	1.7E-35
22888	2459.O23.GZ4 3_357351	AL049301	gi 4500067 emb AL049301.1HSM800086 Homo sapiens mRNA; cDNA DKFZp564P073 (from clone DKFZp564P073)	1.3E-31
22889	2459.P24.GZ4 3_357376	AK018110	gi 12857675 dbj AK018110.1AK018110 Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:633040	1.5E-33

22903	2464.H22.GZ4 3_357870	AB035344	gi 8176599 dbj AB035344.1AB035344S1 Homo sapiens TCL6 gene, exon 1-10b	1.1E-127
22904	2464.I04.GZ4 3_357876	AK025125	gi 10437578 dbj AK025125.1AK025125 Homo sapiens cDNA: FLJ21472 fis, clone COL04936	0
22905	2464.I20.GZ4 3_357892	AK025966	gi 10438647 dbj AK025966.1AK025966 Homo sapiens cDNA: FLJ22313 fis, clone HRC05216	2.8E-61
22909	2464.K18.GZ4 3_357938	AF287938	gi 12656333 gb AF287938.1AF287938 Guichenotia ledifolia NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for	8.3E-44
22912	2464.L15.GZ4 3_357959	AF141308	gi 5737754 gb AF141308.1HSPMFG1 Homo sapiens polyamine modulated factor- 1 (PMF1) gene, exon 1	9.9E-76
22918	2464.P17.GZ4 3_358057	AF052684	gi 2995716 gb AF052684.1HSPRCAD2 Homo sapiens protocadherin 43 gene, exon 2	3E-29
22934	2465.J19.GZ4 3_358299	X02571	gi 31870 emb X02571.1HSGP5MOS Human gene fragment related to oncogene c-mos with Alu repeats (locus gp5, region NV-1)	2.7E-48
22935	2465.K20.GZ4 3_358324	AK019509	gi 12859761 dbj AK019509.1AK019509 Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632435C11, full	2.5E-63
22937	2465.L06.GZ4 3_358334	AK009327	gi 12844057 dbj AK009327.1AK009327 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310012P17, full	7.9E-73
22939	2465.M11.GZ 43_358363	AK022253	gi 10433611 dbj AK022253.1AK022253 Homo sapiens cDNA FLJ12191 fis, clone MAMMA1000843	1.4E-112
22943	2466.B02.GZ4 3_360107	AK023055	gi 10434796 dbj AK023055.1AK023055 Homo sapiens cDNA FLJ12993 fis, clone NT2RP3000197	7.5E-39

22944	2466.C15.GZ4 3_360144	AB013897	gi 6177784 dbj AB013897.1AB013897 Homo sapiens mRNA for HKR1, partial cds	4.3E-53
22945	2466.D19.GZ4 3_360172	AL050141	gi 4884352 emb AL050141.1HSM800441 Homo sapiens mRNA; cDNA DKFZp5860031 (from clone DKFZp5860031)	3.4E-110
22952	2466.I08.GZ4 3_360281	AJ271729	gi 6900103 emb AJ271729.1HSA271729 Homo sapiens mRNA for glucose-regulated protein (HSPA5 gene)	6.2E-72
22953	2466.J01.GZ4 3_360298	AY058527	gi 16197970 gb AY058527.1 Drosophila melanogaster LD23445 full length cDNA	9.4E-40
22954	2466.J24.GZ4 3_360321	AF331425	gi 13375486 gb AF331425.1AF331425 HIV-1 D311 from Australia envelope protein (env) gene, partial cds	1.6E-77
22958	2467.B24.GZ4 3_360513	AJ005821	gi 3123571 emb AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	1.4E-34
22963	2467.H18.GZ4 3_360651	AF036235	gi 2695679 gb AF036235.1AF036235 Gorilla gorilla L1 retrotransposon L1Gg- 1A, complete sequence	2E-169
22964	2467.A03.GZ4 3_360468	BC012960	gi 15277963 gb BC012960.1BC012960 Mus musculus, ring finger protein 12, clone MGC:13712 IMAGE:4193003, mRNA, complete cds	8.7E-36
22965	2467.A05.GZ4 3_360470	BC009113	gi 14318629 gb BC009113.1BC009113 Homo sapiens, clone MGC:18122 IMAGE:4153377, mRNA, complete cds	4.1E-167
22969	2467.G01.GZ4 3_360610	U14573	gi 551542 gb U14573.1HSU14573 ***ALU WARNING: Human Alu-Sq subfamily consensus sequence	2E-61
22971	2467.N22.GZ4 3_360799	AF117756	gi 4530440 gb AF117756.1AF117756 Homo sapiens thyroid hormone receptor- associated protein complex component TRAP150 mRNA, complete	6.8E-77

22973	2467.I12.GZ4 3_360669	AK024049	gi 10436318 dbj AK024049.1AK024049 Homo sapiens cDNA FLJ13987 fis, clone Y79AA1001963, weakly similar to PUTATIVE PRE-MRNA SPLICING	2.1E-47
22977	2467.K14.GZ4 3_360719	AB030001	gi 7416074 dbj AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	7.2E-22
22979	2467.N03.GZ4 3_360780	AK023448	gi 10435386 dbj AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
22980	2467.N07.GZ4 3_360784	AK001931	gi 7023502 dbj AK001931.1AK001931 Homo sapiens cDNA FLJ11069 fis, clone PLACE1004930, highly similar to Homo sapiens MDC-3.13 isofo	2.3E-54
22981	2467.N09.GZ4 3_360786	AE008338	gi 15159908 gb AE008338.1AE008338 Agrobacterium tumefaciens strain C58 linear chromosome, section 142 of 187 of the complete sequen	3.7E-50
22986	2472.C18.GZ4 3_360915	K01921	gi 339606 gb K01921.1HUMTGNB Human Asn-tRNA gene, clone pHt6-2, complete sequence and flanks	3E-29
22992	2472.G03.GZ4 3_360996	AF321082	gi 12958576 gb AF321082.1AF321082 HIV-1 isolate DGOB from France envelope glycoprotein (env) gene, complete cds	5.1E-28
22999	2472.M22.GZ 43_361159	AF338299	gi 12958808 gb AF338299.1AF338299 Amazona ochrocephala auropalliata mitochondrial control region 1, partial sequence	1.4E-145
23002	2472.P22.GZ4 3_361231	AJ330257	gi 15874675 emb AJ330257.1HSA330257 Homo sapiens genomic sequence surrounding NotI site, clone NL1-FA14R	1.1E-63
23005	2473.F08.GZ4 3_361361	AF306355	gi 14573206 gb AF306355.1AF306355 Homo sapiens clone TF3.19 immunoglobulin heavy chain variable region mRNA, partial cds	3.2E-29

23006	2473.F14.GZ4 3_361367	AB050477	gi 11034759 dbj AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	0
23011	2473.I08.GZ4 3_361433	AF224341	gi 15982934 gb AF224341.1AF224341 Mus musculus thiamine transporter 1 (Slc19a2) gene, exons 1 through 6 and complete cds	8.7E-67
23015	2473.O13.GZ4 3_361582	AF203815	gi 6979641 gb AF203815.1AF203815 Homo sapiens alpha gene sequence	5.4E-44
23018	2474.C08.GZ4 3_361673	AK000373	gi 7020417 dbj AK000373.1AK000373 Homo sapiens cDNA FLJ20366 fis, clone HEP18008	5.6E-47
23021	2474.G17.GZ4 3_361778	U75285	gi 2315862 gb U75285.1HSU75285 Homo sapiens apoptosis inhibitor survivin gene, complete cds	1.1E-87
23023	2474.I06.GZ4 3_361815	Z81315	gi 1644298 emb Z81315.1HSF62D4 Human DNA sequence from fosmid F62D4 on chromosome 22q12-qter	2.1E-67
23024	2474.J18.GZ4 3_361851	AF029062	gi 3712662 gb AF029062.1AF029062 Homo sapiens DEAD-box protein (BAT1) gene, partial cds	1.2E-28
23030	2474.P22.GZ4 3_361999	AL050204	gi 4884443 emb AL050204.1HSM800501 Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223)	8.9E-33
23031	2475.A05.GZ4 3_362006	AL109666	gi 5689800 emb AL109666.1IRO35907 Homo sapiens mRNA full length insert cDNA clone EUROIMAGE 35907	6.3E-43
23032	2475.C18.GZ4 3_362067	AK023739	gi 10435762 dbj AK023739.1AK023739 Homo sapiens cDNA FLJ13677 fis, clone PLACE1011982	2.8E-180
23033	2475.E18.GZ4 3_362115	AK024206	gi 10436527 dbj AK024206.1AK024206 Homo sapiens cDNA FLJ14144 fis, clone MAMMA1002909	1.9E-21
23035	2475.H06.GZ4 3_362175	AF322634	gi 12657820 gb AF322634.1AF322634S1 Human herpesvirus 3 strain VZV-Iceland glycoprotein B gene, complete cds	1.2E-173

23036	2475.H13.GZ4 3_362182	AF026853	gi 3882436 gb AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L- 3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2.1E-30
23039	2475.N08.GZ4 3_362321	AK011295	gi 12847322 dbj AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	1.1E-84
23045	2475.M20.GZ 43_362309	AK023843	gi 10435902 dbj AK023843.1AK023843 Homo sapiens cDNA FLJ13781 fis, clone PLACE4000465	8.8E-42
23046	2475.N21.GZ4 3_362334	S45332	gi 255496 gb S45332.1S45332 erythropoietin receptor [human, placental, Genomic, 8647 nt]	1.4E-101
23055	2480.G11.GZ4 3_358658	X83497	gi 603558 emb X83497.1HSLTRERV9 H.sapiens DNA for ZNF80-linked ERV9 long terminal repeat	6.1E-40
23056	2480.H06.GZ4 3_358677	AB002070	gi 12862447 dbj AB002070.1AB002070 Aspergillus clavatus gene for 18S rRNA, partial sequence, strain:NRRL 1	5.5E-28
23061	2480.M20.GZ 43_358811	AL157697	gi 11121002 emb AL157697.1AL157697 Human DNA sequence from clone RP5- 1092C14 on chromosome 6, complete sequence [Homo sapiens]	9.3E-36
23064	2480.P23.GZ4 3_358886	AB037719	gi 7242950 dbj AB037719.1AB037719 Homo sapiens mRNA for KIAA1298 protein, partial cds	3.6E-35
23065	2481.B06.GZ4 3_358917	AK023471	gi 10435415 dbj AK023471.1AK023471 Homo sapiens cDNA FLJ13409 fis, clone PLACE1001716	0
23068	2481.D10.GZ4 3_358969	AL021306	gi 2808416 emb AL021306.1HS1109B5 Human DNA sequence from clone CTB- 1109B5 on chromosome 22 Contains a GSS, complete sequence [Homo	7E-52
23069	2481.D13.GZ4 3_358972	X64467	gi 28579 emb X64467.1HSAALADG H.sapiens ALAD gene for porphobilinogen synthase	4.2E-53

23075	2481.K12.GZ4 3_359139	AK026901	gi 10439868 dbj AK026901.1AK026901 Homo sapiens cDNA: FLJ23248 fis, clone COL03555	5.9E-52
23083	2482.E17.GZ4 3_359384	AK022821	gi 10434440 dbj AK022821.1AK022821 Homo sapiens cDNA FLJ12759 fis, clone NT2RP2001347	9.4E-35
23084	2482.E20.GZ4 3_359387	AK014328	gi 12852104 dbj AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	5.2E-99
23091	2482.N09.GZ4 3_359592	AE008514	gi 15459095 gb AE008514.1AE008514 Streptococcus pneumoniae R6 section 130 of 184 of the complete genome	6.9E-107
23100	2483.J07.GZ4 3_359878	AK022722	gi 10434285 dbj AK022722.1AK022722 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN	1E-300
23101	2483.K02.GZ4 3_359897	AK012908	gi 12849956 dbj AK012908.1AK012908 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810046L04, full	3.7E-189
23106	2483.O07.GZ4 3_359998	AK014328	gi 12852104 dbj AK014328.1AK014328 Mus musculus 14, 17 days embryo head cDNA, RIKEN full-length enriched library, clone:3230401M21,	3.2E-103
23108	2488.C19.GZ4 3_362511	AB023199	gi 4589607 dbj AB023199.1AB023199 Homo sapiens mRNA for KIAA0982 protein, complete cds	1.1E-50
23110	2488.E20.GZ4 3_362560	AK001136	gi 7022203 dbj AK001136.1AK001136 Homo sapiens cDNA FLJ10274 fis, clone HEMBB1001169	1E-35
23111	2488.F06.GZ4 3_362570	AK011295	gi 12847322 dbj AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	8.1E-55
23113	2488.G02.GZ4 3_362590	X15723	gi 31481 emb X15723.1HSFURIN Human fur gene, exons 1 through 8	1.8E-85

23117	2488.K04.GZ4 3_362688	AF026853	gi 3882436 gb AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L- 3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2.1E-30
23122	2489.A03.GZ4 3_362831	AB050477	gi 11034759 dbj AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	6.7E-46
23124	2489.A13.GZ4 3_362841	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	1.8E-178
23127	2489.D18.GZ4 3_362918	AF086310	gi 3483655 gb AF086310.1HUMZD51F08 Homo sapiens full length insert cDNA clone ZD51F08	2.5E-79
23128	2489.F09.GZ4 3_362957	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
23129	2489.G05.GZ4 3_362977	AK023739	gi 10435762 dbj AK023739.1AK023739 Homo sapiens cDNA FLJ13677 fis, clone PLACE1011982	6.8E-209
23140	2489.M11.GZ 43_363127	AE008029	gi 15155994 gb AE008029.1AE008029 Agrobacterium tumefaciens strain C58 circular chromosome, section 87 of 254 of the complete seque	4.2E-44
23144	2490.B06.GZ4 3_363242	AK001915	gi 7023475 dbj AK001915.1AK001915 Homo sapiens cDNA FLJ11053 fis, clone PLACE1004664	1.7E-43
23155	2490.J22.GZ4 3_363450	AF026853	gi 3882436 gb AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L- 3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	2E-30
23160	2490.N24.GZ4 3_363548	AF167438	gi 9622123 gb AF167438.1AF167438 Homo sapiens androgen-regulated short- chain dehydrogenase/reductase 1 (ARSDR1) mRNA, complete cds	8.8E-74
23163	2491.C13.GZ4 3_363657	AK022338	gi 10433714 dbj AK022338.1AK022338 Homo sapiens cDNA FLJ12276 fis, clone MAMMA1001692	6.2E-30

23174	2491.P10.GZ4 3_363966	AJ276936	gi 12214232 emb AJ276936.1NME276936 Neisseria meningitidis partial tbpB gene for transferrin binding protein B subunit, allele 66,	0
23175	2491.P20.GZ4 3_363976	AY027632	gi 15418751 gb AY027632.1 Measles virus strain MVs/Masan.KOR/49.00/2 hemagglutinin (H) mRNA, complete cds	7.8E-283
23177	2496.C08.GZ4 3_364139	U67829	gi 2289943 gb U67829.1HSU67829 Human primary Alu transcript	3.6E-90
23181	2496.F14.GZ4 3_364217	X16983	gi 33945 emb X16983.1HSINTAL4 Human mRNA for integrin alpha-4 subunit	4.7E-53
23183	2496.I06.GZ4 3_364281	BC004138	gi 13278716 gb BC004138.1BC004138 Homo sapiens, ribosomal protein L6, clone MGC:1635 IMAGE:2823733, mRNA, complete cds	8.3E-53
23184	2496.K15.GZ4 3_364338	NM_024711	gi 13376008 ref NM_024711.1 Homo sapiens hypothetical protein FLJ22690 (FLJ22690), mRNA	1.1E-28
23192	2497.E09.GZ4 3_364572	AF284421	gi 15088516 gb AF284421.1AF284421 Homo sapiens complement factor MASP-3 mRNA, complete cds	4.1E-158
23195	2497.J05.GZ4 3_364688	Z56298	gi 1027529 emb Z56298.1HS10C4R H.sapiens CpG island DNA genomic MseI fragment, clone 10c4, reverse read cpg10c4.rtl a	2.5E-42
23199	2497.L05.GZ4 3_364736	AK023448	gi 10435386 dbj AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
23207	2562.B09.GZ4 3_375496	M64241	gi 190813 gb M64241.1HUMQM Human Wilm's tumor-related protein (QM) mRNA, complete cds	3.2E-52
23210	2562.I01.GZ4 3_375656	AF083247	gi 5106788 gb AF083247.1AF083247 Homo sapiens MDG1 mRNA, complete cds	2.4E-48

23214	2562.O01.GZ4 3_375800	AF223389	gi 11066459 gb AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	8.7E-57
23217	2562.H11.GZ4 3_375642	AK023442	gi 10435378 dbj AK023442.1AK023442 Homo sapiens cDNA FLJ13380 fis, clone PLACE1001007	1.7E-64
23218	2562.B24.GZ4 3_375511	AF287932	gi 12656321 gb AF287932.1AF287932 Rayleya bahiensis NADH dehydrogenase subunit F (ndhF) gene, partial cds; chloroplast gene for chl	1.8E-31
23229	2498.A02.GZ4 3_364853	AY031766	gi 13738569 gb AY031766.1 HIV-1 isolate NC5203-1999 from USA pol polyprotein (pol) gene, partial cds	1.3E-29
23230	2498.A19.GZ4 3_364870	AL122114	gi 6102936 emb AL122114.1HSM801274 Homo sapiens mRNA; cDNA DKFZp434K0221 (from clone DKFZp434K0221); partial cds	1E-59
23235	2498.G15.GZ4 3_365010	M86752	gi 184564 gb M86752.1HUMIEF Human transformation-sensitive protein (IEF SSP 3521) mRNA, complete cds	3.4E-54
23238	2498.I17.GZ4 3_365060	AJ335654	gi 15880072 emb AJ335654.1HSA335654 Homo sapiens genomic sequence surrounding NotI site, clone NR5-IJ21R	4.3E-41
23239	2498.K20.GZ4 3_365111	X15940	gi 36129 emb X15940.1HSRPL31 Human mRNA for ribosomal protein L31	1.7E-25
23240	2498.M19.GZ 43_365158	AF203815	gi 6979641 gb AF203815.1AF203815 Homo sapiens alpha gene sequence	4E-47
23242	2498.P07.GZ4 3_365218	AF410975	gi 15553753 gb AF410975.1AF410975 Measles virus genotype D4 strain MVi/Montreal.CAN/12.89 hemagglutinin gene, complete cds	3.5E-29
23244	2507.C03.GZ4 3_366992	NM_025080	gi 13376633 ref NM_025080.1 Homo sapiens hypothetical protein FLJ22316 (FLJ22316), mRNA	1E-232
23259	2511.J18.GZ4 3_369643	M81806	gi 184406 gb M81806.1HUMHSPQZ7 Human housekeeping (Q1Z 7F5) gene, exons 2 through 7, complete cds	4.7E-34

23261	2499.A22.GZ4 3_365257	AK024860	gi 10437268 dbj AK024860.1AK024860 Homo sapiens cDNA: FLJ21207 fis, clone COL00362	6.4E-49
23263	2499.C09.GZ4 3_365292	AJ330464	gi 15874882 emb AJ330464.1HSA330464 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IL7C	3.3E-100
23268	Clu1009284.1	AF026853	gi 3882436 gb AF026853.1HSHADHSC 1 Homo sapiens mitochondrial short-chain L- 3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	1.3E-30
23269	Clu1022935.2	AL590711.7	gi 16304966 emb AL590711.7AL590711 Human DNA sequence from clone RP11- 284O18 on chromosome 9, complete sequence [Homo sapiens]	3.9E-118
23270	Clu1037152.1	M87652	gi 182743 gb M87652.1HUMFPRPR Human formylpeptide receptor gene, promoter region	1.1E-21
23271	Clu13903.1	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	1.5E-293
23272	Clu139979.2	AB056828	gi 13365953 dbj AB056828.1AB056828 Macaca fascicularis brain cDNA clone:QfIA-13447, full insert sequence	1.4E-33
23274	Clu187860.2	AL050204	gi 4884443 emb AL050204.1HSM800501 Homo sapiens mRNA; cDNA DKFZp586F1223 (from clone DKFZp586F1223)	4.7E-33
23275	Clu189993.1	AB030001	gi 7416074 dbj AB030001.1AB030001 Homo sapiens gene for SGRF, complete cds	9.6E-87
23276	Clu20975.1	AF039687	gi 3170173 gb AF039687.1AF039687 Homo sapiens antigen NY-CO-1 (NY-CO- 1) mRNA, complete cds	2.7E-190
23278	Clu218833.1	AF223389	gi 11066459 gb AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	1E-139

23279	Clu244504.2	Z59663	gi 1031576 emb Z59663.1HS168F9F H.sapiens CpG island DNA genomic MseI fragment, clone 168F9, forward read cpg168f9.ft1a	7.5E-22
23281	Clu376516.1	AK018003	gi 12857525 dbj AK018003.1AK018003 Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830450H20, full	1.7E-63
23282	Clu376630.1	U93571	gi 2072968 gb U93571.1HSU93571 Human L1 element L1.24 p40 gene, complete cds	8.7E-291
23283	Clu377044.2	AK024860	gi 10437268 dbj AK024860.1AK024860 Homo sapiens cDNA: FLJ21207 fis, clone COL00362	1.6E-49
23284	Clu379689.1	BC007110	gi 13937991 gb BC007110.1BC007110 Homo sapiens, clone MGC:14768 IMAGE:4291902, mRNA, complete cds	0
23286	Clu387530.4	AK009770	gi 12844769 dbj AK009770.1AK009770 Mus musculus adult male tongue cDNA, RIKEN full-length enriched library, clone:2310043C14, full	1.5E-80
23287	Clu388450.2	AK023448	gi 10435386 dbj AK023448.1AK023448 Homo sapiens cDNA FLJ13386 fis, clone PLACE1001104, weakly similar to MYOSIN HEAVY CHAIN, NON-MU	0
23288	Clu396325.1	Z78727	gi 1508005 emb Z78727.1HSPA15B9 H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA15B9	1.2E-38
23291	Clu400258.1	AB038971	gi 12862672 dbj AB038971.1AB038965S7 Homo sapiens CFLAR gene, exon 10, exon 11	4E-74
23293	Clu402591.3	AF170811	gi 6715105 gb AF170811.1AF170811 Homo sapiens CaBP2 (CABP2) gene, complete cds	7E-26

23295	Clu404081.2	AK011443	gi 12847570 dbj AK011443.1AK011443 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610018B07, full ins	5E-153
23297	Clu41346.1	AB042029	gi 16326128 dbj AB042029.1AB042029 Homo sapiens DEPC-1 mRNA for prostate cancer antigen-1, complete cds	0
23299	Clu416124.1	AK000293	gi 7020278 dbj AK000293.1AK000293 Homo sapiens cDNA FLJ20286 fis, clone HEP04358	3.3E-34
23300	Clu417672.1	AK027667	gi 14042514 dbj AK027667.1AK027667 Homo sapiens cDNA FLJ14761 fis, clone NT2RP3003302	1.6E-183
23301	Clu423664.1	AF287270	gi 9844925 gb AF287270.1AF287270 Homo sapiens mucolipin (MCOLN1) gene, complete cds	6.3E-34
23303	Clu442923.3	BC014256	gi 15559816 gb BC014256.1BC014256 Homo sapiens, Similar to guanine nucleotide binding protein (G protein), beta polypeptide 2-like	1.5E-236
23304	Clu446975.1	AL022342.6	gi 7159715 emb AL022342.6HS29M10 Human DNA sequence from clone RP1- 29M10 on chromosome 20, complete sequence [Homo sapiens]	1.8E-74
23305	Clu449839.2	BC001607	gi 12804410 gb BC001607.1BC001607 Homo sapiens, clone IMAGE:3543874, mRNA, partial cds	1.9E-27
23306	Clu449889.1	S45332	gi 255496 gb S45332.1S45332 erythropoietin receptor [human, placental, Genomic, 8647 nt]	8E-101
23307	Clu451707.2	AJ004862	gi 4038586 emb AJ004862.1HSAJ4862 Homo sapiens partial MUC5B gene, exon 1- 29	4.7E-49
23308	Clu454509.3	AK022973	gi 10434673 dbj AK022973.1AK022973 Homo sapiens cDNA FLJ12911 fis, clone NT2RP2004425, highly similar to Mus musculus axotrophin mR	1.7E-285

23310	Clu455862.1	AK023951	gi 10436049 dbj AK023951.1AK023951 Homo sapiens cDNA FLJ13889 fis, clone THYRO1001595	3.3E-27
23311	Clu460493.1	AK012865	gi 12849888 dbj AK012865.1AK012865 Mus musculus 10, 11 days embryo cDNA, RIKEN full-length enriched library, clone:2810036K01, full	1.7E-57
23314	Clu470032.1	AF223389	gi 11066459 gb AF223389.1AF223389 Homo sapiens PCGEM1 gene, non-coding mRNA	1.2E-116
23317	Clu477271.1	BC007307	gi 13938350 gb BC007307.1BC007307 Homo sapiens, Similar to zinc finger protein 268, clone IMAGE:3352268, mRNA, partial cds	4.6E-56
23318	Clu480410.1	AK000713	gi 7020973 dbj AK000713.1AK000713 Homo sapiens cDNA FLJ20706 fis, clone KAIA1273	0
23320	Clu497138.1	AF270579	gi 9755121 gb AF270579.1AF270579 Homo sapiens clone 18ptel_481c6 sequence	3.8E-29
23321	Clu498886.1	U49973	gi 2226003 gb U49973.1HSU49973 Human Tigger1 transposable element, complete consensus sequence	1.4E-24
23323	Clu5013.2	BC007458	gi 13938610 gb BC007458.1BC007458 Homo sapiens, clone MGC:12217 IMAGE:3828631, mRNA, complete cds	0
23324	Clu5105.2	AL512712	gi 12224956 emb AL512712.1HSM80291 5 Homo sapiens mRNA; cDNA DKFZp761J139 (from clone DKFZp761J139)	0
23325	Clu510539.2	AK023812	gi 10435860 dbj AK023812.1AK023812 Homo sapiens cDNA FLJ13750 fis, clone PLACE3000331	1.4E-32
23326	Clu514044.1	AJ403947	gi 14270388 emb AJ403947.1HSA403947 Homo sapiens partial SLC22A3 gene for organic cation transporter 3, exon 2	4.4E-295

23329	Clu520370.1	AF093016	gi 5579305 gb AF093016.1AF093016 Homo sapiens 22k48 gene, 5'UTR	7.3E-67
23330	Clu524917.1	AL1573620	gi 15028613 emb AL157362.10AL157362 Human DNA sequence from clone RP11- 142D16 on chromosome 13q14.3-21.31, complete sequence [Homo	4.9E-23
23331	Clu528957.1	AB060919	gi 13874604 dbj AB060919.1AB060919 Macaca fascicularis brain cDNA clone:QtrA-14728, full insert sequence	1.5E-31
23334	Clu540142.2	AJ005821	gi 3123571 emb AJ005821.1HSA5821 Homo sapiens mRNA for X-like 1 protein	3.5E-36
23335	Clu540379.2	AF088011	gi 3523217 gb AF088011.1HUMYY75G1 0 Homo sapiens full length insert cDNA clone YY75G10	2.4E-49
23336	Clu549507.1	U14571	gi 551540 gb U14571.1HSU14571 ***ALU WARNING: Human Alu-Sc subfamily consensus sequence	1.6E-48
23339	Clu556827.3	AB038163	gi 10280537 dbj AB038163.1AB038163 Homo sapiens NDUFV3 gene for mitochondrial NADH-Ubiquinone oxidoreductase, complete cds	9.7E-22
23340	Clu558569.2	AF061258	gi 3108092 gb AF061258.1AF061258 Homo sapiens LIM protein mRNA, complete cds	1E-300
23343	Clu570804.1	AK023843	gi 10435902 dbj AK023843.1AK023843 Homo sapiens cDNA FLJ13781 fis, clone PLACE4000465	4.4E-42
23344	Clu572170.2	U18271	gi 885681 gb U18271.1HSTMPO6 Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for t	4.9E-57
23346	Clu587168.1	AJ276804	gi 10803412 emb AJ276804.1HSA276804 Homo sapiens mRNA for protocadherin (PCDHX gene)	5.8E-69
23347	Clu588996.1	U73166	gi 1613889 gb U73166.1U73166 Homo sapiens cosmid clone LUCA15 from 3p21.3, complete sequence	9.3E-22

23349	Clu598388.1	AF327178	gi 11878341 gb AF327178.1AF327178 Homo sapiens clone 20ptel_cA35_21t7 sequence	1.1E-26
23350	Clu604822.2	AB063021	gi 14388457 dbj AB063021.1AB063021 Macaca fascicularis brain cDNA clone:QmoA-11389, full insert sequence	2.6E-65
23353	Clu627263.1	AK021759	gi 10433005 dbj AK021759.1AK021759 Homo sapiens cDNA FLJ11697 fis, clone HEMBA1005035	5.7E-30
23356	Clu641662.2	AL157697	gi 11121002 emb AL157697.11AL157697 Human DNA sequence from clone RP5- 1092C14 on chromosome 6, complete sequence [Homo sapiens]	7E-84
23358	Clu6712.1	AK024029	gi 10436287 dbj AK024029.1AK024029 Homo sapiens cDNA FLJ13967 fis, clone Y79AA1001402, weakly similar to Homo sapiens paraneoplasti	0
23361	Clu685244.2	S56773	gi 298606 gb S56773.1S56773 putative serine-threonine protein kinase {3' UTR, Alu repeats} [human, Genomic, 1470 nt]	1.1E-35
23362	Clu691653.1	D28126	gi 559316 dbj D28126.1HUMATPSAS Human gene for ATP synthase alpha subunit, complete cds (exon 1 to 12)	6.3E-37
23367	Clu709796.2	AB070013	gi 15207866 dbj AB070013.1AB070013 Macaca fascicularis testis cDNA clone:QtsA-11243, full insert sequence	8.4E-118
23369	Clu727966.1	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
23372	Clu756337.1	BC004923	gi 13436241 gb BC004923.1BC004923 Homo sapiens, clone IMAGE:3605104, mRNA, partial cds	4.1E-250
23376	Clu823296.3	AK023179	gi 10434987 dbj AK023179.1AK023179 Homo sapiens cDNA FLJ13117 fis, clone NT2RP3002660	6.4E-33

23377	Clu830453.2	AK027301	gi 14041890 dbj AK027301.1AK027301 Homo sapiens cDNA FLJ14395 fis, clone HEMBA1003250, weakly similar to PROTEIN KINASE APK1A (EC 2	0
23378	Clu839006.1	AB023199	gi 4589607 dbj AB023199.1AB023199 Homo sapiens mRNA for KIAA0982 protein, complete cds	3.3E-51
23379	Clu847088.1	AL078632.6	gi 6002309 emb AL078632.6HSA255N20 Human DNA sequence from clone 255N20 on chromosome 22, complete sequence [Homo sapiens]	4.2E-40
23380	Clu853371.2	S79349	gi 1110571 gb S79349.1S79349 Homo sapiens type 1 iodothyronine deiodinase (hdiol) gene, partial cds	1.6E-48
23381	Clu88462.1	AF026855	gi 3882438 gb AF026855.1HSHADHSC 3 Homo sapiens mitochondrial short-chain L- 3-hydroxyacyl-CoA dehydrogenase (HADHSC) gene, nuclear	1.1E-65
23382	Clu935908.2	AK025271	gi 10437753 dbj AK025271.1AK025271 Homo sapiens cDNA: FLJ21618 fis, clone COL07487	8.2E-54
23386	DTT00087024 .1	AF036235	gi 2695679 gb AF036235.1AF036235 Gorilla gorilla L1 retrotransposon L1Gg- 1A, complete sequence	0
23387	DTT00089020 .1	AF324172	gi 12958747 gb AF324172.1AF324172 Dictyophora indusiata strain ASI 32001 internal transcribed spacer 1, partial sequence; 5.8S ribo	1.1E-142
23388	DTT00171014 .1	AB050477	gi 11034759 dbj AB050477.1AB050477 Homo sapiens NIBAN mRNA, complete cds	0
23389	DTT00514029 .1	BC001978	gi 12805042 gb BC001978.1BC001978 Homo sapiens, clone IMAGE:3461487, mRNA, partial cds	6E-284

23390	DTT00740010 .1	AF216292	gi 7229461 gb AF216292.1AF216292 Homo sapiens endoplasmic reticulum luminal Ca ²⁺ binding protein grp78 mRNA, complete cds	9.5E-229
23391	DTT00945030 .1	AL117237	gi 5834563 emb AL117237.1HS328E191 Novel human gene mapping to chromosome 1	0
23394	DTT01315010 .1	X16983	gi 33945 emb X16983.1HSINTAL4 Human mRNA for integrin alpha-4 subunit	0
23395	DTT01503016 .1	AK025473	gi 10437996 dbj AK025473.1AK025473 Homo sapiens cDNA: FLJ21820 fis, clone HEP01232	0
23396	DTT01555018 .1	AE007613	gi 15023874 gb AE007613.1AE007613 Clostridium acetobutylicum ATCC824 section 101 of 356 of the complete genome	0
23397	DTT01685047 .1	M54985	gi 177005 gb M54985.1GIBBGLOETA H.lar psi-eta beta-like globin pseudogene, exon 1,2,3	6.8E-107
23398	DTT01764019 .1	AF307053	gi 12018057 gb AF307053.1AF307053 Thermococcus litoralis sugar kinase, trehalose/maltose binding protein (malE), trehalose/maltose	0
23401	DTT02367007 .1	AK001580	gi 7022920 dbj AK001580.1AK001580 Homo sapiens cDNA FLJ10718 fis, clone NT2RP3001096, weakly similar to Rattus norvegicus leprecan	0
23402	DTT02671007 .1	AF384048	gi 14488027 gb AF384048.1AF384048 Homo sapiens interferon kappa precursor gene, complete cds	1.8E-170
23403	DTT02737017 .1	AF182418	gi 10197635 gb AF182418.1AF182418 Homo sapiens MDS017 (MDS017) mRNA, complete cds	9E-207
23404	DTT02850005 .1	AK011295	gi 12847322 dbj AK011295.1AK011295 Mus musculus 10 days embryo cDNA, RIKEN full-length enriched library, clone:2610002L04, full ins	2.5E-141

23406	DTT03037029 .1	AE006916	gi 13879055 gb AE006916.1AE006916 Mycobacterium tuberculosis CDC1551, section 2 of 280 of the complete genome	2.1E-129
23407	DTT03150008 .1	M83822	gi 1580780 gb M83822.1HUMCDC4REL Human beige-like protein (BGL) mRNA, partial cds	0
23408	DTT03367008 .1	NM_01209 0.2	gi 15011903 ref NM_01209.2 Homo sapiens actin cross-linking factor (ACF7), transcript variant 1, mRNA	0
23411	DTT03913023 .1	AK018110	gi 12857675 dbj AK018110.1AK018110 Mus musculus adult male medulla oblongata cDNA, RIKEN full-length enriched library, clone:633040	2E-214
23412	DTT03978010 .1	BC015529	gi 15930193 gb BC015529.1BC015529 Homo sapiens, Similar to ribose 5- phosphate isomerase A, clone MGC:9441 IMAGE:3904718, mRNA, comp	0
23413	DTT04070014 .1	L43411	gi 893273 gb L43411.1HUM25DC1Z Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence	4E-102
23414	DTT04084010 .1	AF259790	gi 12240019 gb AF259790.1AF259790 Desulfitobacterium sp. PCE-1 o- chlorophenol reductive dehalogenase (cprA) gene, complete cds	2.2E-288
23415	DTT04160007 .1	AF338299	gi 12958808 gb AF338299.1AF338299 Amazona ochrocephala auropalliata mitochondrial control region 1, partial sequence	1.4E-181
23417	DTT04378009 .1	AF102129	gi 5922722 gb AF102129.1AF102129 Rattus norvegicus KPL2 (Kpl2) mRNA, complete cds	4.7E-146
23418	DTT04403013 .1	AE007580	gi 15023517 gb AE007580.1AE007580 Clostridium acetobutylicum ATCC824 section 68 of 356 of the complete genome	1.5E-199
23420	DTT04660017 .1	NM_02507 9	gi 13376631 ref NM_02507.1 Homo sapiens hypothetical protein FLJ23231 (FLJ23231), mRNA	0

23421	DTT04956054 .1	AF050179	gi 3319283 gb AF050179.1AF050179 Homo sapiens CENP-C binding protein (DAXX) mRNA, complete cds	0
23422	DTT04970018 .1	AK015635	gi 12854041 dbj AK015635.1AK015635 Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930486L24, full	1.4E-84
23424	DTT05571010 .1	AB014533	gi 3327079 dbj AB014533.1AB014533 Homo sapiens mRNA for KIAA0633 protein, partial cds	1.8E-53
23426	DTT05742029 .1	AF344987	gi 13448249 gb AF344987.1AF344987 Hepatitis C virus isolate RDpostSC1c2 polyprotein gene, partial cds	0
23427	DTT06137030 .1	AY049285	gi 15146287 gb AY049285.1 Arabidopsis thaliana AT3g58570/F14P22_160 mRNA, complete cds	2.2E-143
23428	DTT06161014 .1	AJ330465	gi 15874883 emb AJ330465.1HSA330465 Homo sapiens genomic sequence surrounding NotI site, clone NR1-IM15C	2.5E-28
23429	DTT06706019 .1	AF226787	gi 12407487 gb AF226787.1AF226787 Syrrhopodon confertus ribulose-1,5- bisphosphate carboxylase large subunit (rbcL) gene, partial cd	0
23430	DTT06837021 .1	AK000658	gi 7020892 dbj AK000658.1AK000658 Homo sapiens cDNA FLJ20651 fis, clone KAT01814	0
23431	DTT07040015 .1	AF047347	gi 3005557 gb AF047347.1AF047347 Homo sapiens adaptor protein X11alpha mRNA, complete cds	0
23432	DTT07088009 .1	AF326517	gi 15080738 gb AF326517.1AF326517 Abies grandis pinene synthase gene, partial cds	0
23433	DTT07182014 .1	AB035187	gi 9955412 dbj AB035187.1AB035187 Homo sapiens RHD gene, intron 1, complete sequence	3.1E-84

23434	DTT07405044 .1	AP002946	gi 16267254 dbj AP002946.1AP002946 Mastacembelus favus mitochondrial DNA, complete genome	0
23435	DTT07408020 .1	AE008061	gi 15156405 gb AE008061.1AE008061 Agrobacterium tumefaciens strain C58 circular chromosome, section 119 of 254 of the complete sequ	6.9E-245
23438	DTT08005024 .1	U18270	gi 885679 gb U18270.1HSTMPO4 Human thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	5.1E-108
23439	DTT08098020 .1	AF387946	gi 15021617 gb AF387946.1AF387946 Homo sapiens clone J102 melanocortin 1 receptor gene, promoter region	0
23440	DTT08167018 .1	NM_020642 2	gi 11034852 ref NM_020642.1 Homo sapiens chromosome 11 open reading frame 17 (C11orf17), mRNA	1E-183
23441	DTT08249022 .1	M86752	gi 184564 gb M86752.1HUMIEF Human transformation-sensitive protein (IEF SSP 3521) mRNA, complete cds	0
23443	DTT08514022 .1	AK001927	gi 7023494 dbj AK001927.1AK001927 Homo sapiens cDNA FLJ11065 fis, clone PLACE1004868, weakly similar to MALE STERILITY PROTEIN 2	0
23444	DTT08527013 .1	AF271388	gi 8515842 gb AF271388.1AF271388 Homo sapiens CMP-N-acetylneuraminic acid synthase mRNA, complete cds	0
23445	DTT08595020 .1	L07758	gi 177764 gb L07758.1HUM56KDAPR Human IEF SSP 9502 mRNA, complete cds	0
23446	DTT08711019 .1	D87930	gi 2443337 dbj D87930.1D87930 Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)	0
23447	DTT08773020 .1	X15187	gi 37260 emb X15187.1HSTRA1 Human tra1 mRNA for human homologue of murine tumor rejection antigen gp96	6.8E-298

23448	DTT08874012 .1	AK026442	gi 10439307 dbj AK026442.1AK026442 Homo sapiens cDNA: FLJ22789 fis, clone KAIA2171	0
23449	DTT09387018 .1	AF273672	gi 15186755 gb AF273672.1AF273672 Mus musculus RANBP9 isoform 1 (Ranbp9) mRNA, complete cds	0
23450	DTT09396022 .1	AK000913	gi 7021874 dbj AK000913.1AK000913 Homo sapiens cDNA FLJ10051 fis, clone HEMBA1001281	0
23452	DTT09604016 .1	AK022722	gi 10434285 dbj AK022722.1AK022722 Homo sapiens cDNA FLJ12660 fis, clone NT2RM4002174, moderately similar to MRP PROTEIN	2.2E-198
23454	DTT09742009 .1	AF025409	gi 2582414 gb AF025409.1AF025409 Homo sapiens zinc transporter 4 (ZNT4) mRNA, complete cds	0
23455	DTT09753017 .1	L03532	gi 187280 gb L03532.1HUMM4PRO Human M4 protein mRNA, complete cds	5.7E-58
23456	DTT09793019 .1	AK025125	gi 10437578 dbj AK025125.1AK025125 Homo sapiens cDNA: FLJ21472 fis, clone COL04936	0
23457	DTT09796028 .1	AF272390	gi 8705239 gb AF272390.1AF272390 Homo sapiens myosin 5c (MYO5C) mRNA, complete cds	0
23459	DTT10360040 .1	AJ133798	gi 6453351 emb AJ133798.1HSA133798 Homo sapiens mRNA for copine VI protein	0
23460	DTT10539016 .1	AF152924	gi 5453323 gb AF152924.1AF152924 Mus musculus syntaxin4-interacting protein synip mRNA, complete cds	2.6E-70
23461	DTT10564022 .1	AF322634	gi 12657820 gb AF322634.1AF322634S1 Human herpesvirus 3 strain VZV-Iceland glycoprotein B gene, complete cds	0
23462	DTT10683041 .1	X69392	gi 36114 emb X69392.1HSRP26AA H.sapiens mRNA for ribosomal protein L26	3E-250

23463	DTT10819011 .1	U14568	gi 551537 gb U14568.1HSU14568 ***ALU WARNING: Human Alu-Sb subfamily consensus sequence	2.6E-93
23465	DTT11479018 .1	AF309561	gi 10954043 gb AF309561.1AF309561 Homo sapiens KRAB zinc finger protein ZFQR mRNA, complete cds	0
23466	DTT11483012 .1	U57053	gi 1616674 gb U57053.1HSU57053 Human unconventional myosin-ID (MYO1F) gene, partial cds	3.1E-245
23467	DTT11548015 .1	X05332	gi 35740 emb X05332.1HSPSAR Human mRNA for prostate specific antigen	0
23468	DTT11730017 .1	U14572	gi 551541 gb U14572.1HSU14572 ***ALU WARNING: Human Alu-Sp subfamily consensus sequence	4.7E-90
23471	DTT11902028 .1	AK001915	gi 7023475 dbj AK001915.1AK001915 Homo sapiens cDNA FLJ11053 fis, clone PLACE1004664	0
23472	DTT11915017 .1	U66062	gi 1724068 gb U66062.1HSU66062 Human glp-1 receptor gene, promoter region and partial cds	5.9E-111
23475	DTT12201062 .1	M73791	gi 189265 gb M73791.1HUMNOVGENE Human novel gene mRNA, complete cds	0
23476	DTT12470020 .1	AK026618	gi 10439509 dbj AK026618.1AK026618 Homo sapiens cDNA: FLJ22965 fis, clone KAT10418	0

Example 96:Members of Protein Families

SEQ ID NOS: 22001-23477 were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table 149 (inserted prior to claims) provides: 1) the SEQ ID NO ("SEQ ID") of the query polynucleotide sequence; 2) the sequence name ("SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("PFAM ID") of the the protein family profile hit; 4) a brief description of the profile hit ("PFAM DESCRIPTION"); 5) the

score ("SCORE") of the profile hit; 6) the starting nucleotide of the profile hit ("START"); and 7) the ending nucleotide of the profile hit ("END").

Table 149

SEQ ID	SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
22007	2504.C11.GZ43_365848	PF00179	Ubiquitin-conjugating enzyme	92.64	4	159
22010	2504.E23.GZ43_365908	PF01260	AP endonuclease family 1	88.28	222	481
22046	2505.G16.GZ43_36633 3	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	263	495
22109	2510.N14.GZ43_36935 1	PF02348	Cytidyltransferase	187.84	357	675
22126	2365.D10.GZ43_34530 8	PF01018	GTP1/OBG family	96.12	50	507
22134	2365.F24.GZ43_345370	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	120.2	251	522
22189	2366.L21.GZ43_345942	PF00612	IQ calmodulin-binding motif	33.96	415	477
22189	2366.L21.GZ43_345942	PF00063	Myosin head (motor domain)	207.12	8	369
22259	2368.O03.GZ43_34671 7	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	120.2	242	513
22267	2535.C23.GZ43_370158	PF02114	Phosducin	32	152	589
22334	2537.D11.GZ43_37093 8	PF00083	Sugar (and other) transporter	122.88	4	288
22335	2537.D20.GZ43_37094 7	PF00131	Metallothionein	48.56	563	665
22349	2537.N12.GZ43_37117 9	PF01352	KRAB box	123.24	313	498
22363	2538.B03.GZ43_371266	PF00160	Cyclophilin type peptidyl-prolyl cis-trans isomerase	117.68	320	591
22391	2554.A06.GZ43_37585 3	PF03015	Male sterility protein	44.96	605	749
22394	2554.A16.GZ43_37586 3	PF02348	Cytidyltransferase	195.48	397	650
22405	2554.I10.GZ43_376049	PF03041	lef-2	31.88	479	536

			Ubiquinol-cytochrome C reductase complex 14kD			
22419	2565.B15.GZ43_398171	PF02271	subunit	70.76	29	188
22422	2565.C17.GZ43_398204	PF00089	Trypsin	45.28	5	110
22482	2540.I17.GZ43_372216	PF00023	Ank repeat	75.44	444	542
22507	2541.L08.GZ43_372663	PF00499	NADH-ubiquinone/plastoquinone oxidoreductase chain 6	54.72	89	237
22514	2506.C15.GZ43_366620	PF00076	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	44.44	70	276
22521	2506.G24.GZ43_366725	PF00096	Zinc finger, C2H2 type	46.68	156	224
22527	2506.J20.GZ43_366793	PF00595	PDZ domain (Also known as DHR or GLGF).	34.16	290	502
22543	2542.D19.GZ43_372866	PF00098	Zinc knuckle	46.68	224	276
22563	2542.N21.GZ43_373108	PF01545	Cation efflux family	42.24	191	325
22569	2555.F16.GZ43_373295	PF02348	Cytidyltransferase	215.04	357	713
22716	2560.H21.GZ43_375268	PF00510	Cytochrome c oxidase subunit III	37.28	224	436
22721	2560.K10.GZ43_375329	PF01018	GTP1/OBG family	104.56	50	573
22759	2561.O17.GZ43_376584	PF00826	Ribosomal L10	79.88	46	180
22766	2456.B12.GZ43_355864	PF01545	Cation efflux family	34.16	102	236
22771	2456.D04.GZ43_355904	PF02114	Phosducin	30.52	139	576
22813	2457.J23.GZ43_356451	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	189	421
22818	2457.L21.GZ43_356497	PF00023	Ank repeat	38	208	306
22910	2464.L02.GZ43_357946	PF00076	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	34.84	244	350

22914	2464.N05.GZ43_35799 7	PF00023	Ank repeat	128.28	491	589
22935	2465.K20.GZ43_35832 4	PF02594	Uncharacterized ACR, YggU family COG1872	77.64	210	442
22952	2466.I08.GZ43_360281	PF00012	Hsp70 protein	120.92	16	208
22967	2467.D10.GZ43_36054 7	PF00008	EGF-like domain	31.04	63	113
23002	2472.P22.GZ43_361231	PF00499	NADH- ubiquinone/plastoquinone oxidoreductase chain 6	64.72	81	209
23011	2473.I08.GZ43_361433	PF00895	ATP synthase protein 8	66.88	5	148
23039	2475.N08.GZ43_36232 1	PF00804	Syntaxin	53.08	226	601
23051	2480.D13.GZ43_35858 8	PF03025	Papillomavirus E5	33.56	583	749
23065	2481.B06.GZ43_358917	PF00098	Zinc knuckle	35.88	79	133
23100	2483.J07.GZ43_359878	PF00142	4Fe-4S iron sulfur cluster binding proteins, NifH/frxC family	32.8	211	288
23101	2483.K02.GZ43_35989 7	PF00160	Cyclophilin type peptidyl- prolyl cis-trans isomerase	117.52	244	516
23107	2488.B07.GZ43_362475	PF01260	AP endonuclease family 1	79.88	251	614
23128	2489.F09.GZ43_362957	PF02348	Cytidylyltransferase	174.36	347	591
23183	2496.I06.GZ43_364281	PF02790	Cytochrome C oxidase subunit II, transmembrane domain	45.8	131	242
23207	2562.B09.GZ43_375496	PF00826	Ribosomal L10	106.28	49	341
23216	2562.E14.GZ43_375573	PF00023	Ank repeat	87.04	230	328
23225	2562.H18.GZ43_37564 9	PF02594	Uncharacterized ACR, YggU family COG1872	65.44	206	437
23244	2507.C03.GZ43_366992	PF00083	Sugar (and other) transporter	95.52	107	355
23267	2499.I09.GZ43_365436	PF00160	Cyclophilin type peptidyl- prolyl cis-trans isomerase	43.24	139	238

In addition, SEQ ID NOS:23478-23568 were also used to conduct a profile search as

described above. Several of the polypeptides of the invention were found to have characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table 150 (inserted prior to claims) provides: 1) the SEQ ID NO ("SEQ ID") of the query protein sequence; 2) the sequence name ("PROTEIN SEQ NAME") used as an internal identifier of the query sequence; 3) the accession number ("PFAM ID") of the the protein family profile hit; 4) a brief description of the profile hit ("PFAM DESCRIPTION"); 5) the score ("SCORE") of the profile hit; 6) the starting residue of the profile hit ("START"); and 7) the ending residue of the profile hit ("END").

Some SEQ ID NOS exhibited multiple profile hits where the query sequence contains overlapping profile regions, and/or where the sequence contains two different functional domains. Each of the profile hits of Tables 8 and 9 is described in more detail below. The acronyms for the profiles (provided in parentheses) are those used to identify the profile in the Pfam, Prosite, and InterPro databases. The Pfam database can be accessed through web sites supported by Genome Sequencing Center at the Washington University School of Medicine or by the European Molecular Biology Laboratories in Heidelberg, Germany. The Prosite database can be accessed at the ExPASy Molecular Biology Server on the internet. The InterPro database can be accessed at a web site supported by the EMBL European Bioinformatics Institute. The public information available on the Pfam, Prosite, and InterPro databases regarding the various profiles, including but not limited to the activities, function, and consensus sequences of various proteins families and protein domains, is incorporated herein by reference.

Table 150

SEQ ID	PROTEIN SEQ NAME	PFAM ID	PFAM DESCRIPTION	SCORE	START	END
23481	DTP00514038.1	PF00587	tRNA synthetase class II core domain (G, H, P, S and T)	33.42	1	116
23482	DTP00740019.1	PF00012	Hsp70 protein	948.22	27	564
23484	DTP01169031.1	PF00023	Ank repeat	159.66	82	114
23484	DTP01169031.1	PF00023	Ank repeat	159.66	181	213

23484	DTP01169031.1	PF00023	Ank repeat	159.66	148	180
23484	DTP01169031.1	PF00023	Ank repeat	159.66	115	147
23484	DTP01169031.1	PF00023	Ank repeat	159.66	82	114
23484	DTP01169031.1	PF00023	Ank repeat	159.66	49	81
23484	DTP01169031.1	PF00023	Ank repeat	159.66	16	48
23484	DTP01169031.1	PF00023	Ank repeat	159.66	181	213
23484	DTP01169031.1	PF00023	Ank repeat	159.66	115	147
23484	DTP01169031.1	PF00023	Ank repeat	159.66	49	81
23484	DTP01169031.1	PF00023	Ank repeat	159.66	16	48
23484	DTP01169031.1	PF00023	Ank repeat	159.66	148	180
23486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	427	479
23486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	49	111
23486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	248	300
23486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	303	362
23486	DTP01315019.1	PF01839	FG-GAP repeat	255.09	365	424
23495	DTP02737026.1	PF01423	Sm protein	31.6	19	66
23496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
23496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
23496	DTP02850014.1	PF00804	Syntaxin	156.59	1	292
23510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	80	116
23510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	38	74
23510	DTP04403022.1	PF00400	WD domain, G-beta repeat	35.93	1	33
23512	DTP04660026.1	PF00083	Sugar (and other) transporter	234.43	1	484
23512	DTP04660026.1	PF00083	Sugar (and other) transporter	234.43	1	484
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	105	208
23518	DTP05742038.1	PF01018	GTP1/OBG family	133.76	7	97
23519	DTP06137039.1	PF02271	Ubiquinol-cytochrome C reductase complex 14kD subunit	141.38	4	154
23521	DTP06706028.1	PF00054	Laminin G domain	63.34	56	178
23521	DTP06706028.1	PF00054	Laminin G domain	63.34	281	292

23523	DTP07040024.1	PF00640	Phosphotyrosine interaction domain (PTB/PID).	233.89	461	618
23523	DTP07040024.1	PF00595	PDZ domain (Also known as DHR or GLGF).	85.47	656	742
23532	DTP08249031.1	PF00515	TPR Domain	115	4	37
23532	DTP08249031.1	PF00515	TPR Domain	115	72	105
23532	DTP08249031.1	PF00515	TPR Domain	115	38	71
23532	DTP08249031.1	PF00515	TPR Domain	115	259	292
23532	DTP08249031.1	PF00515	TPR Domain	115	300	333
23532	DTP08249031.1	PF00515	TPR Domain	115	225	258
23535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
23535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
23535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
23535	DTP08527022.1	PF02348	Cytidylyltransferase	48.59	1	166
23536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	183	221
23536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	236	273
23536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	365	402
23536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	279	316
23536	DTP08595029.1	PF00400	WD domain, G-beta repeat	80.04	325	357
23537	DTP08711028.1	PF00023	Ank repeat	81.96	22	54
23537	DTP08711028.1	PF00023	Ank repeat	81.96	55	87
23538	DTP08773029.1	PF00183	Hsp90 protein	100.71	104	173
23540	DTP09387027.1	PF00069	Protein kinase domain	224.56	76	342
23545	DTP09742018.1	PF01545	Cation efflux family	368.71	114	418
23545	DTP09742018.1	PF01545	Cation efflux family	368.71	114	418
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	879	899
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	856	876
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	831	851
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	808	828
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	780	800
23548	DTP09796037.1	PF00612	IQ calmodulin-binding motif	87.63	757	777
23548	DTP09796037.1	PF01843	DIL domain	125.23	1574	1679
23548	DTP09796037.1	PF00063	Myosin head (motor domain)	1228.24	69	741
23550	DTP10360049.1	PF00168	C2 domain	50.07	26	114
23550	DTP10360049.1	PF00168	C2 domain	50.07	228	315

23551	DTP10539025.1	PF00595	PDZ domain (Also known as DHR or GLGF).	32.34	5	84
23553	DTP10683050.1	PF00467	KOW motif	89.22	49	107
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	402	424
23556	DTP11479027.1	PF01352	KRAB box	134.58	8	70
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	374	396
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	346	368
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	318	340
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	290	312
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	262	284
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	234	256
23556	DTP11479027.1	PF00096	Zinc finger, C2H2 type	209.31	206	228
23557	DTP11483021.1	PF00063	Myosin head (motor domain)	339.24	117	271
23557	DTP11483021.1	PF00063	Myosin head (motor domain)	339.24	34	115
23558	DTP11548024.1	PF00089	Trypsin	272.53	25	253
23564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
23564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
23564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
23564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
23564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
23564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
23564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
23564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
23564	DTP11966049.1	PF00023	Ank repeat	165.68	181	214
23564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48
23564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
23564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
23564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48
23564	DTP11966049.1	PF00023	Ank repeat	165.68	148	180
23564	DTP11966049.1	PF00023	Ank repeat	165.68	115	147
23564	DTP11966049.1	PF00023	Ank repeat	165.68	82	114
23564	DTP11966049.1	PF00023	Ank repeat	165.68	49	81
23564	DTP11966049.1	PF00023	Ank repeat	165.68	16	48
23566	DTP12201071.1	PF00826	Ribosomal L10	467.36	1	176
23566	DTP12201071.1	PF00826	Ribosomal L10	467.36	1	176

Example 97: Detection of Differential Expression Using Arrays and source of patient tissue samples

mRNA isolated from samples of cancerous and normal breast, colon, and prostate tissue obtained from patients were analyzed to identify genes differentially expressed in cancerous and normal cells. Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001).

Table 151 (inserted prior to claims) provides information about each patient from which colon tissue samples were isolated, including: the Patient ID ("PT ID") and Path ReportID ("Path ID"), which are numbers assigned to the patient and the pathology reports for identification purposes; the group ("Grp") to which the patients have been assigned; the anatomical location of the tumor ("Anatom Loc"); the primary tumor size ("Size"); the primary tumor grade ("Grade"); the identification of the histopathological grade ("Histo Grade"); a description of local sites to which the tumor had invaded ("Local Invasion"); the presence of lymph node metastases ("Lymph Met"); the incidence of lymph node metastases (provided as a number of lymph nodes positive for metastasis over the number of lymph nodes examined) ("Lymph Met Incid"); the regional lymphnode grade ("Reg Lymph Grade"); the identification or detection of metastases to sites distant to the tumor and their location ("Dist Met & Loc"); the grade of distant metastasis ("Dist Met Grade"); and general comments about the patient or the tumor ("Comments"). Histopathology of all primary tumors indicated the tumor was adenocarcinoma except for Patient ID Nos. 130 (for which no information was provided), 392 (in which greater than 50% of the cells were mucinous carcinoma), and 784 (adenosquamous carcinoma). Extranodal extensions were described in three patients, Patient ID Nos. 784, 789, and 791. Lymphovascular invasion was described in Patient ID Nos. 128, 278, 517, 534, 784, 786, 789, 791, 890, and 892. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Table 152 below provides information about each patient from which the prostate

tissue samples were isolated, including: 1) the “Patient ID”, which is a number assigned to the patient for identification purposes; 2) the “Tissue Type”; and 3) the “Gleason Grade” of the tumor. Histopathology of all primary tumors indicated the tumor was adenocarcinoma.

Table 152. Prostate patient data.

Patient ID	Tissue Type	Gleason Grade	Patient ID	Tissue Type	Gleason Grade
93	Prostate Cancer	3+4	391	Prostate Cancer	3+3
94	Prostate Cancer	3+3	420	Prostate Cancer	3+3
95	Prostate Cancer	3+3	425	Prostate Cancer	3+3
96	Prostate Cancer	3+3	428	Prostate Cancer	4+3
97	Prostate Cancer	3+2	431	Prostate Cancer	3+4
100	Prostate Cancer	3+3	492	Prostate Cancer	3+3
101	Prostate Cancer	3+3	493	Prostate Cancer	3+4
104	Prostate Cancer	3+3	496	Prostate Cancer	3+3
105	Prostate Cancer	3+4	510	Prostate Cancer	3+3
106	Prostate Cancer	3+3	511	Prostate Cancer	4+3
138	Prostate Cancer	3+3	514	Prostate Cancer	3+3
151	Prostate Cancer	3+3	549	Prostate Cancer	3+3
153	Prostate Cancer	3+3	552	Prostate Cancer	3+3
155	Prostate Cancer	4+3	858	Prostate Cancer	3+4
171	Prostate Cancer	3+4	859	Prostate Cancer	3+4
173	Prostate Cancer	3+4	864	Prostate Cancer	3+4
231	Prostate Cancer	3+4	883	Prostate Cancer	4+4
232	Prostate Cancer	3+3	895	Prostate Cancer	3+3
251	Prostate Cancer	3+4	901	Prostate Cancer	3+3
282	Prostate Cancer	4+3	909	Prostate Cancer	3+3
286	Prostate Cancer	3+3	921	Prostate Cancer	3+3
294	Prostate Cancer	3+4	923	Prostate Cancer	4+3
351	Prostate Cancer	5+4	934	Prostate Cancer	3+3
361	Prostate Cancer	3+3	1134	Prostate Cancer	3+4
362	Prostate Cancer	3+3	1135	Prostate Cancer	3+3
365	Prostate Cancer	3+2	1136	Prostate Cancer	3+4
368	Prostate Cancer	3+3	1137	Prostate Cancer	3+3
379	Prostate Cancer	3+4	1138	Prostate Cancer	4+3
388	Prostate Cancer	5+3			

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Table 153 provides information about each patient from which the breast tissue samples were isolated, including: 1) the “Pat Num”, a number assigned to the patient for identification purposes; 2) the “Histology”, which indicates whether the tumor was characterized as an intraductal carcinoma (IDC) or ductal carcinoma in situ (DCIS); 3) the

incidence of lymph node metastases (LMF), represented as the number of lymph nodes positive to metastases out of the total number examined in the patient; 4) the "Tumor Size"; 5) "TNM Stage", which provides the tumor grade (T#), where the number indicates the grade and "p" indicates that the tumor grade is a pathological classification; regional lymph node metastasis (N#), where "0" indicates no lymph node metastases were found, "1" indicates lymph node metastases were found; and "X" means information not available and; the identification or detection of metastases to sites distant to the tumor and their location (M#), with "X" indicating that no distant metastases were reported; and the stage of the tumor ("Stage Grouping"). "nr" indicates "no reported".

10 **Table 153** Breast cancer patient data

Pat Num	Histology	LMF	Tumor Size	TNM Stage	Stage Grouping
280	IDC, DCIS+D2	nr	2 cm	T2NXMX	probable Stage II
284	IDC, DCIS	0/16	2 cm	T2pN0MX	Stage II
285	IDC, DCIS	nr	4.5 cm	T2NXMX	probable Stage II
291	IDC, DCIS	0/24	4.5 cm	T2pN0MX	Stage II
302	IDC, DCIS	nr	2.2 cm	T2NXMX	probable Stage II
375	IDC, DCIS	nr	1.5 cm	T1NXMX	probable Stage I
408	IDC	0/23	3.0 cm	T2pN0MX	Stage II
416	IDC	0/6	3.3 cm	T2pN0MX	Stage II
421	IDC, DCIS	nr	3.5 cm	T2NXMX	probable Stage II
459	IDC	2/5	4.9 cm	T2pN1MX	Stage II
465	IDC	0/10	6.5 cm	T3pN0MX	Stage II
470	IDC, DCIS	0/6	2.5 cm	T2pN0MX	Stage II
472	IDC, DCIS	6/45	5.0+ cm	T3pN1MX	Stage III
474	IDC	0/18	6.0 cm	T3pN0MX	Stage II
476	IDC	0/16	3.4 cm	T2pN0MX	Stage II
605	IDC, DCIS	1/25	5.0 cm	T2pN1MX	Stage II
649	IDC, DCIS	1/29	4.5 cm	T2pN1MX	Stage II

Identification of differentially expressed genes

cDNA probes were prepared from total RNA isolated from the patient cells described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

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Total RNA was first reverse transcribed into cDNA using a primer containing a T7

RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, *e.g.*, Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.

Each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array.

Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample.

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by

incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is

truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

Table 154 (inserted prior to claims) provides the results for gene products expressed by at least 2-fold or greater in cancerous prostate, colon, or breast tissue samples relative to normal tissue samples in at least 20% of the patients tested. Table 154 includes: 1) the SEQ ID NO ("SEQ ID") assigned to each sequence for use in the present specification; 2) the Cluster Identification No. ("CLUSTER"); 3) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was at least 2-fold greater in cancerous breast tissue than in matched normal tissue ("BREAST PATIENTS $\geq 2x$ "); 4) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was less than or equal to $\frac{1}{2}$ of the expression level in matched normal breast cells ("BREAST PATIENTS $\leq \text{halfx}$ "); 5) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was at least 2-fold greater in cancerous colon tissue than in matched normal tissue ("COLON PATIENTS $\geq 2x$ "); 6) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was less than or equal to $\frac{1}{2}$ of the expression level in matched normal colon cells ("COLON PATIENTS $\leq \text{halfx}$ "); 7) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was at least 2-fold greater in cancerous prostate tissue than in matched normal tissue ("PROSTATE PATIENTS $\geq 2x$ "); and 8) the percentage of patients tested in which expression levels (e.g., as message level) of the gene was less than or equal to $\frac{1}{2}$ of the expression level in matched normal prostate cells ("PROSTATE PATIENTS $\leq \text{halfx}$ ").

These data provide evidence that the genes represented by the polynucleotides having the indicated sequences are differentially expressed in breast cancer as compared to normal non-cancerous breast tissue, are differentially expressed in colon cancer as compared to normal non-cancerous colon tissue, and are differentially expressed in prostate cancer as compared to normal non-cancerous prostate tissue.

Table 154

SEQ ID	CLONE ID	BREAST	BREAST	COLON	COLON	PROSTATE	PROSTATE
		PATIENTS ≥2x	PATIENTS ≤halfx	PATIENTS ≥2x	PATIENTS ≤halfx	PATIENTS ≥2x	PATIENTS ≤halfx
22004	M00072944A:C07				35		
22008	M00072947B:G04				32.5		
22009	M00072947D:G0						
	5				27.5		
22015	M00072963B:G11				40		
22016	M00072967A:G0						
	7				25		
22018	M00072968A:F08				22.5		
22020	M00072968D:E05				32.5		
22021	M00072970C:B07				25		
22024	M00072971C:B07				22.5		
22028	M00072975A:D1						
	1	23.5					
22034	M00073001A:F07				27.5		
22038	M00073003A:E06				42.5		
22039	M00073003B:E10				27.5		
22042	M00073006A:H0						
	8	23.5					
22043	M00073006C:D07				27.5		
22045	M00073009B:C08				32.5		52.4
22048	M00073013A:D1						
	0				32.5		
22049	M00073013A:F10				20		
22050	M00073013C:B10				32.5		
22052	M00073014D:F01				40		
22054	M00073015A:H0						
	6				47.5		
22061	M00073020C:F07				32.5		
22062	M00073020D:C06			37.5			
22063	M00073021C:E04				30		
22071	M00073030B:C02				22.5		
22072	M00073030C:A02				20		
22073	M00073036C:H10				25		

22086	M00073043D:H0 9				32.5		
22090	M00073044C:G12				32.5		
22094	M00073045C:E06				22.5		
22096	M00073045D:B04				30		
22105	M00073048C:B01				20		
22107	M00073049A:H0 4				27.5		49.2
22108	M00073049B:B03		23.5		40		31.7
22109	M00073049B:B06				20		
22110	M00073049C:C09				20		
22136	M00073066C:D02				27.5		
22142	M00073070B:B06				32.5		
22146	M00073074D:A0 4				20		
22153	M00073086D:B05				30		
22156	M00073091B:C04				20		
22163	M00073424D:C03	52.9					
22171	M00073403C:C10				30		
22173	M00073403C:E11	29.4			52.5		
22176	M00073412C:E07				30		
22177	M00073435C:E06				27.5		
22178	M00073412D:B07		35.3	42.5			
22189	M00073430C:B02				32.5		
22196	M00073442A:F07				25		
22197	M00073442B:D12				27.5		20.6
22199	M00073446C:A03				22.5		
22201	M00073447D:F01				45		38.1
22204	M00073453C:C09	41.2					
22212	M00073469B:A09				27.5		36.5
22216	M00073474C:F08				30		22.2
22220	M00073484B:A05		23.5		30		22.2
22228	M00073497C:D03		29.4	30			
22233	M00073513A:G0 7	23.5				25.4	

22236	M00073517A:A0 6				32.5		
22241	M00073529A:F03				20		
22242	M00073530B:A02				20		54.0
22243	M00073531B:H02						50.8
22246	M00073539C:H05				27.5		
22247	M00073541B:C10				30		
22248	M00073547B:F04				22.5		
22249	M00073547C:D02				35		
22256	M00073554B:D11				37.5		
22264	M00073568A:G0 6				32.5		
22265	M00073568C:G07				25		
22269	M00073576B:E03				22.5		
22270	M00073576C:C11				20		
22273	M00073580A:D0 8				32.5		
22280	M00073598D:E11				40		
22284	M00073601D:D0 8				32.5		
22286	M00073603B:C03			30			
22288	M00073603C:C02		76.5		67.5		
22290	M00073604B:B07				30		
22294	M00073605B:F11		58.8				
22299	M00073614C:F06			60			
22300	M00073615D:E03				82.5		
22301	M00073616A:F06				32.5		28.6
22304	M00073621D:A0 4				27.5		
22316	M00073633D:A0 4		23.5	52.5			
22318	M00073634C:H08	23.5			85	39.7	
22319	M00073635D:C10		35.3				
22323	M00073638A:A1 2			47.5			

22325	M00073639A:G0 8				27.5		
22340	M00073651C:F06	29.4			27.5		36.5
22342	M00073652D:B11		64.7		70		
22343	M00073655B:A04			37.5			
22353	M00073669A:F04				20		
22354	M00073669B:E12	23.5		27.5			
22357	M00073687A:D1 1			50		22.2	
22361	M00073672D:E09				35		42.9
22367	M00073677B:F01				32.5		
22369	M00073678B:H02			35			
22372	M00073681A:F12		29.4				25.4
22377	M00073689C:C09						41.3
22382	M00073696C:D11		35.3				
22384	M00073697C:F11		29.4				34.9
22388	M00073700B:D12				30		
22390	M00073708D:E10						23.8
22392	M00073709B:F01				25		
22394	M00073709C:A02				22.5		
22398	M00073713D:E07				27.5		
22399	M00073715A:F05				20		31.7
22400	M00073715B:B06				37.5		27.0
22401	M00073717C:A12				37.5		
22403	M00073720D:H1 1				27.5		20.6
22408	M00073735C:E04						23.8
22413	M00073743C:F03				25		
22417	M00073748B:F07				35		
22424	M00073754B:D05				37.5		
22436	M00073765A:E02				32.5		
22439	M00073766B:B07				22.5		
22442	M00073772B:E07						22.2
22450	M00073779B:B11				32.5		

22462	M00073798A:H0 3				35		
22464	M00073801B:A10				35		
22467	M00073809C:E09		23.5	45		25.4	
22469	M00073813D:B06						27.0
22470	M00073814C:B04						71.4
22473	M00073790A:A1 2						36.5
22480	M00073799A:G0 2				37.5		
22481	M00073799D:G0 4				30		
22486	M00073813A:E06				32.5		
22487	M00073813B:A01				30		
22493	M00073822C:E02				35		
22494	M00073824A:C04						38.1
22497	M00073832A:A0 6				20		20.6
22500	M00073834A:H1 0				35		
22502	M00073834D:H0 6				25		31.7
22503	M00073836D:E05					23.8	
22506	M00073838B:F09				25		
22509	M00073839A:D0 5		23.5		47.5		41.3
22513	M00073850A:H0 9						54.0
22532	M00073867D:F10						36.5
22533	M00073871B:C12				32.5		
22534	M00073872C:B09				22.5		
22535	M00073872D:B01				32.5		
22536	M00073872D:E10				22.5		
22544	M00073883B:D03				22.5		
22550	M00073892B:F12				32.5		
22555	M00073905B:A03						55.6

22562	M00073897B:B11			30		
	M00073899A:D0					
22564	6			32.5		
22565	M00073911B:G10					23.8
22567	M00073916A:B07			42.5		23.8
22572	M00073923C:A04	29.4		22.5		
22575	M00073931D:E02			27.5		
22577	M00073936D:E05			25		
22579	M00073908C:D09			40		27.0
	M00073944D:A0					
22599	7			27.5		
22620	M00073968B:B06			27.5		57.1
22625	M00073979C:G07			37.5		44.4
22634	M00073988D:F09					38.1
22641	M00073979B:B05			27.5		66.7
22645	M00073988C:G08			40		
22654	M00074011D:C05			42.5		
22656	M00074013C:C09			20		
22659	M00074015A:C03			22.5		
	M00074020D:G1					
22665	0			40		
22669	M00074025A:F06			25		36.5
22670	M00074025B:A12					20.6
22671	M00074026C:H09			32.5		
22687	M00074053C:E05	25.0	30			
22695	M00074059B:G10			27.5		
22703	M00074075B:A09		27.5			
22706	M00074079A:E07			42.5		31.7
22708	M00074084D:B04					33.3
22710	M00074085B:E06					23.8
22712	M00074087B:C09					28.6
22713	M00074087C:G05					23.8
22717	M00074089D:E03			20		54.0
22720	M00074093B:A03	23.5	27.5			
22722	M00074094B:F10					52.4

22723	M00074096D:G1 2						25.4
22726	M00074098C:B09						23.8
22727	M00074099C:B09				20		
22729	M00074101D:D0 7			35			
22730	M00074102A:C04				37.5		
22733	M00074107C:C08				35		
22741	M00074131A:H0 9				37.5		27.0
22742	M00074132C:F10				32.5		22.2
22747	M00074138D:A0 8				45		22.2
22749	M00074142B:C11				32.5		
22750	M00074142D:A1 0				22.5		
22753	M00074122A:B02				37.5		
22756	M00074132A:E11			22.5			
22757	M00074132B:B07				35		20.6
22758	M00074134A:G1 1				27.5		
22759	M00074149A:B10		41.2	47.5			
22762	M00074153D:A0 5				37.5		
22765	M00074157C:G08				25		
22767	M00074158C:F12				37.5		
22769	M00074159C:A05				25		
22777	M00074174A:C02				27.5		27.0
22782	M00074177B:H08				35		
22785	M00074179C:B01				27.5		28.6
22787	M00074184D:B01				37.5		28.6
22789	M00074191C:D08						57.1
22790	M00074192C:C10						33.3
22793	M00074198C:A12	29.4			45		31.7
22794	M00074198D:D1 0						36.5

22800	M00074203D:F01				40		
	M00074206A:H1						
22802	2				40		22.2
22806	M00074208B:F09				22.5		41.3
22811	M00074215A:F09				42.5		
	M00074216D:H0						
22813	3				35		
22819	M00074223B:D12				30		
	M00074225A:H1						
22821	2				25		
22827	M00074234A:C05				30		
22830	M00074234D:F12				37.5		
22834	M00074242D:F09				25		
22837	M00074247B:G11				27.5		
22839	M00074248C:E12					25.4	
22840	M00074249C:B11				27.5		
22846	M00074251C:E03				35		
22849	M00074253C:F03				32.5		
22850	M00074255B:A01				20		
	M00074258A:H1						
22851	2				32.5		
22861	M00074271B:E11				25		
	M00074280D:H0						
22869	3				20		31.7
22870	M00074284B:B03				27.5		25.4
22873	M00074288A:F11				45		20.6
	M00074290A:G1						
22874	0				37.5		
22875	M00074290C:B05						20.6
22877	M00074293D:B05				20		
	M00074293D:H0						
22878	7				32.5		
22882	M00074304B:C09				22.5		39.7
	M00074304D:D0						
22883	7						36.5
22884	M00074306A:B09				27.5		

22886	M00074310D:D0 2				35		25.4
22888	M00074315B:A03				22.5		
22892	M00074835A:H1 0				40		
22893	M00074835B:F12				22.5		
22895	M00074837A:E01				35		
22899	M00074843D:D0 2				25		65.1
22900	M00074844B:B02	58.8	20				
22901	M00074844D:F09				30		20.6
22905	M00074847B:G03				30		
22909	M00074852B:A02		37.5				
22912	M00074854A:C11				40		
22913	M00074855B:A05				27.5		
22917	M00074863D:F07				27.5		
22919	M00074317D:B08						20.6
22920	M00074320C:A06						54.0
22921	M00074865A:F05				20		50.8
22923	M00074871C:G05				20		
22926	M00074879A:A0 2				35		22.2
22930	M00074890A:E03				20		20.6
22931	M00074895D:H1 2						20.6
22934	M00074901C:E05				27.5		
22938	M00074905D:A0 1				35		30.2
22941	M00074912B:A10						65.1
22943	M00074916A:H0 3				30		
22949	M00074927D:G0 9				22.5		
22954	M00074936B:E10				37.5		
22955	M00074939B:A06				32.5		
22959	M00074966D:E08						34.9

22962	M00074974C:E11					22.2
22964	M00074954A:H0 6			20		
22975	M00072985A:C12			20		
22981	M00072996B:A10			27.5		20.6
22984	M00072997D:H0 6			40		20.6
22986	M00074333D:A1 1	41.2	47.5			
22990	M00074343C:A03			30		
22998	M00074366A:H0 7			27.5		42.9
23004	M00074392C:D02			32.5		
23006	M00074417D:F07	23.5	67.5			
23008	M00074406B:F10			27.5		
23012	M00074391B:D02		27.5			
23019	M00074461D:E04			47.5		25.4
23025	M00074488C:C08			32.5		
23027	M00074501A:G0 7					49.2
23029	M00074515A:E02				25.4	
23030	M00074515C:A11			32.5		
23031	M00074516B:H03					23.8
23032	M00074525A:B05					20.6
23039	M00074561D:D1 2			30	28.6	
23040	M00074566B:A04			35		
23044	M00074555A:E10			27.5		
23045	M00074561A:B09			40		
23052	M00074582D:B09					25.4
23057	M00074596D:B12			20		22.2
23058	M00074606C:G02	29.4				
23064	M00074628C:D03			37.5		
23067	M00074637A:C02			20		
23068	M00074638D:C12	29.4		35		
23069	M00074639A:C08			30		

23073	M00074662B:A05		35.3			
23078	M00074676D:H0 7			22.5		
23080	M00074681D:A0 2			32.5		
23082	M00074699B:C03			32.5		
23083	M00074701D:H0 9			25		
23086	M00074713B:F02			20		39.7
23089	M00074723D:D0 5			27.5		
23092	M00074740B:F06			27.5		
23095	M00074752A:D0 8			32.5		20.6
23099	M00074765D:F06			40		
23102	M00074773C:G03			20		
23103	M00074774A:D0 3					31.7
23105	M00074780C:C02			20		
23110	M00075000A:D0 6			32.5		
23117	M00074800B:H01			35		
23120	M00074825C:E06			30		
23122	M00075018A:G0 4			30		
23134	M00075035C:C09			32.5		
23135	M00075045D:H0 3			25		
23145	M00075153C:C11			22.5		
23146	M00075161A:E05			30		
23152	M00075152D:C06			30		
23155	M00075160A:E04			42.5		
23163	M00075174D:D0 6			27.5		
23167	M00075199D:D1 1		29.4			36.5

23168	M00075201D:A0 5				30		
23169	M00075203A:G0 6				35		20.6
23179	M00075245A:A0 6		41.2	37.5		28.6	
23189	M00075283A:F04					34.9	
23198	M00075329B:E10		25.0	62.5			
23203	M00075344D:A0 8				22.5		
23224	M00075379A:E07				27.5		
23225	M00075383A:B11				25		
23227	M00075409A:E04				25		
23235	M00075448B:G11				35		20.6
23239	M00075460C:B06		35.3	62.5		20.6	
23245	M00075504B:A10				32.5		
23250	M00075514A:G1 2				32.5		
23266	M00075621A:F06				20		20.6
23386		23.5					
23387				34.3			
23388			23.5	67.5			
23390		35.3		26.1			
23400					32.5		
23402							41.3
23403							
23404					30.0	28.6	
23426				36.6			
23427					42.9		38.2
23429					31.6		
23434				55.0			
23438					21.3		21.5
23439					30.0		
23444							
23445				27.5			

23447		29.4		32.6			
23449		35.3		60.9			
23461			29.4				
23462			41.2	36.2			
23463					27.5		
23472					23.4		
23474					37.5		
23475			35.3	54.3			

Example 98: Antisense Regulation of Gene Expression

The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells can be further analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

Methods for analysis using antisense technology are well known in the art. For example, a number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target are designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh, RNAture, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors considered when designing antisense oligonucleotides include: 1) the The expression of the differentially expressed genes represented by the polynucleotides in the cancerous cells can be analyzed using antisense knockout technology to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting a metastatic phenotype.

A number of different oligonucleotides complementary to the mRNA generated by the differentially expressed genes identified herein can be designed as potential antisense oligonucleotides, and tested for their ability to suppress expression of the genes. Sets of antisense oligomers specific to each candidate target are designed using the sequences of the polynucleotides corresponding to a differentially expressed gene and the software program HYBsimulator Version 4 (available for Windows 95/Windows NT or for Power Macintosh,

RNAture, Inc. 1003 Health Sciences Road, West, Irvine, CA 92612 USA). Factors that are considered when designing antisense oligonucleotides include: 1) the secondary structure of oligonucleotides; 2) the secondary structure of the target gene; 3) the specificity with no or minimum cross-hybridization to other expressed genes; 4) stability; 5) length and 6) terminal GC content. The antisense oligonucleotide is designed so that it will hybridize to its target sequence under conditions of high stringency at physiological temperatures (*e.g.*, an optimal temperature for the cells in culture to provide for hybridization in the cell, *e.g.*, about 37°C), but with minimal formation of homodimers.

Using the sets of oligomers and the HYBsimulator program, three to ten antisense oligonucleotides and their reverse controls are designed and synthesized for each candidate mRNA transcript, which transcript is obtained from the gene corresponding to the target polynucleotide sequence of interest. Once synthesized and quantitated, the oligomers are screened for efficiency of a transcript knock-out in a panel of cancer cell lines. The efficiency of the knock-out is determined by analyzing mRNA levels using lightcycler quantification. The oligomers that resulted in the highest level of transcript knock-out, wherein the level was at least about 50%, preferably about 80-90%, up to 95% or more up to undetectable message, are selected for use in a cell-based proliferation assay, an anchorage independent growth assay, and an apoptosis assay.

The ability of each designed antisense oligonucleotide to inhibit gene expression is tested through transfection into LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate carcinoma cells. For each transfection mixture, a carrier molecule (such as a lipid, lipid derivative, lipid-like molecule, cholesterol, cholesterol derivative, or cholesterol-like molecule) is prepared to a working concentration of 0.5 mM in water, sonicated to yield a uniform solution, and filtered through a 0.45 μ m PVDF membrane. The antisense or control oligonucleotide is then prepared to a working concentration of 100 μ M in sterile Millipore water. The oligonucleotide is further diluted in OptiMEM™ (Gibco/BRL), in a microfuge tube, to 2 μ M, or approximately 20 μ g oligo/ml of OptiMEM™. In a separate microfuge tube, the carrier molecule, typically in the amount of about 1.5-2 nmol carrier/ μ g antisense oligonucleotide, is diluted into the same volume of OptiMEM™ used to dilute the oligonucleotide. The diluted antisense oligonucleotide is immediately added to the diluted carrier and mixed by pipetting up and down. Oligonucleotide is added to the cells to a final

concentration of 30 nM.

The level of target mRNA that corresponds to a target gene of interest in the transfected cells is quantitated in the cancer cell lines using the Roche LightCycler™ real-time PCR machine. Values for the target mRNA are normalized versus an internal control (*e.g.*, beta-actin). For each 20 µl reaction, extracted RNA (generally 0.2-1 µg total) is placed into a sterile 0.5 or 1.5 ml microcentrifuge tube, and water is added to a total volume of 12.5 µl. To each tube is added 7.5 µl of a buffer/enzyme mixture, prepared by mixing (in the order listed) 2.5 µl H₂O, 2.0 µl 10X reaction buffer, 10 µl oligo dT (20 pmol), 1.0 µl dNTP mix (10 mM each), 0.5 µl RNAsin® (20u) (Ambion, Inc., Hialeah, FL), and 0.5 µl MMLV reverse transcriptase (50u) (Ambion, Inc.). The contents are mixed by pipetting up and down, and the reaction mixture is incubated at 42°C for 1 hour. The contents of each tube are centrifuged prior to amplification.

An amplification mixture is prepared by mixing in the following order: 1X PCR buffer II, 3 mM MgCl₂, 140 µM each dNTP, 0.175 pmol each oligo, 1:50,000 dil of SYBR® Green, 0.25 mg/ml BSA, 1 unit *Taq* polymerase, and H₂O to 20 µl. (PCR buffer II is available in 10X concentration from Perkin-Elmer, Norwalk, CT). In 1X concentration it contains 10 mM Tris pH 8.3 and 50 mM KCl. SYBR® Green (Molecular Probes, Eugene, OR) is a dye which fluoresces when bound to double stranded DNA. As double stranded PCR product is produced during amplification, the fluorescence from SYBR® Green increases. To each 20 µl aliquot of amplification mixture, 2 µl of template RT is added, and amplification is carried out according to standard protocols. The results are expressed as the percent decrease in expression of the corresponding gene product relative to non-transfected cells, vehicle-only transfected (mock-transfected) cells, or cells transfected with reverse control oligonucleotides.

Example 99: Effect of Expression on Proliferation

The effect of gene expression on the inhibition of cell proliferation can be assessed in metastatic breast cancer cell lines (MDA-MB-231 ("231")); SW620 colon colorectal carcinoma cells; SKOV3 cells (a human ovarian carcinoma cell line); or LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells.

Cells are plated to approximately 60-80% confluency in 96-well dishes. Antisense or reverse control oligonucleotide is diluted to 2 µM in OptiMEM™. The oligonucleotide-OptiMEM™ can then be added to a delivery vehicle, which delivery vehicle can be selected so

as to be optimized for the particular cell type to be used in the assay. The oligo/delivery vehicle mixture is then further diluted into medium with serum on the cells. The final concentration of oligonucleotide for all experiments can be about 300 nM.

Antisense oligonucleotides are prepared as described above. Cells are transfected overnight at 37°C and the transfection mixture is replaced with fresh medium the next morning. Transfection is carried out as described above 8.

Those antisense oligonucleotides that result in inhibition of proliferation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit proliferation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of proliferation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit proliferation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

Example 100: Effect of Gene Expression on Cell Migration

The effect of gene expression on the inhibition of cell migration can be assessed in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells using static endothelial cell binding assays, non-static endothelial cell binding assays, and transmigration assays.

For the static endothelial cell binding assay, antisense oligonucleotides are prepared as described above. Two days prior to use, prostate cancer cells (CaP) are plated and transfected with antisense oligonucleotide as described above. On the day before use, the medium is replaced with fresh medium, and on the day of use, the medium is replaced with fresh medium containing 2 μ M CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min. Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in DMEM/1% BSA/ 10 mM HEPES pH 7.0. Finally, CaP cells are counted and resuspended at a concentration of 1×10^6 cells/ml.

Endothelial cells (EC) are plated onto 96-well plates at 40-50% confluence 3 days prior to use. On the day of use, EC are washed 1X with PBS and 50 μ l DMEM/1%BSA/10mM

HEPES pH 7 is added to each well. To each well is then added 50K (50 λ) CaP cells in DMEM/1% BSA/ 10mM HEPES pH 7. The plates are incubated for an additional 30 min and washed 5X with PBS containing Ca⁺⁺ and Mg⁺⁺. After the final wash, 100 μ L PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

5 For the non-static endothelial cell binding assay, CaP are prepared as described above. EC are plated onto 24-well plates at 30-40% confluence 3 days prior to use. On the day of use, a subset of EC are treated with cytokine for 6 hours then washed 2X with PBS. To each well is then added 150-200K CaP cells in DMEM/1% BSA/ 10mM HEPES pH 7. Plates are placed on a rotating shaker (70 RPM) for 30 min and then washed 3X with PBS containing Ca⁺⁺ and
10 Mg⁺⁺. After the final wash, 500 μ L PBS is added to each well and fluorescence is read on a fluorescent plate reader (Ab492/Em 516 nm).

For the transmigration assay, CaP are prepared as described above with the following changes. On the day of use, CaP medium is replaced with fresh medium containing 5 μ M CellTracker green CMFDA (Molecular Probes, Inc.) and cells are incubated for 30 min.

15 Following incubation, CaP medium is replaced with fresh medium (no CMFDA) and cells are incubated for an additional 30-60 min. CaP cells are detached using CMF PBS/2.5 mM EDTA or trypsin, spun and resuspended in EGM-2-MV medium. Finally, CaP cells are counted and resuspended at a concentration of 1x10⁶ cells/ml.

EC are plated onto FluorBlok transwells (BD Biosciences) at 30-40% confluence 5-7
20 days before use. Medium is replaced with fresh medium 3 days before use and on the day of use. To each transwell is then added 50K labeled CaP. 30 min prior to the first fluorescence reading, 10 μ g of FITC-dextran (10K MW) is added to the EC plated filter. Fluorescence is then read at multiple time points on a fluorescent plate reader (Ab492/Em 516 nm).

Those antisense oligonucleotides that result in inhibition of binding of LNCaP, PC3,
25 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells to endothelial cells indicate that the corresponding gene plays a role in the production or maintenance of the cancerous phenotype in cancerous prostate cells. Those antisense oligonucleotides that result in inhibition of endothelial cell transmigration by LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 prostate cancer cells indicate that the corresponding gene plays a role in the production or maintenance
30 of the cancerous phenotype in cancerous prostate cells.

Example 101: Effect of Gene Expression on Colony Formation

The effect of gene expression upon colony formation of SW620 cells, SKOV3 cells, MD-MBA-231 cells, LNCaP cells, PC3 cells, 22Rv1 cells, MDA-PCA-2b cells, and DU145 cells can be tested in a soft agar assay. Soft agar assays are conducted by first establishing a bottom layer of 2 ml of 0.6% agar in media plated fresh within a few hours of layering on the cells. The cell layer is formed on the bottom layer by removing cells transfected as described above from plates using 0.05% trypsin and washing twice in media. The cells are counted in a Coulter counter, and resuspended to 10^6 per ml in media. 10 μ l aliquots are placed with media in 96-well plates (to check counting with WST1), or diluted further for the soft agar assay. 2000 cells are plated in 800 μ l 0.4% agar in duplicate wells above 0.6% agar bottom layer. After the cell layer agar solidifies, 2 ml of media is dribbled on top and antisense or reverse control oligo (produced as described above) is added without delivery vehicles. Fresh media and oligos are added every 3-4 days. Colonies form in 10 days to 3 weeks. Fields of colonies are counted by eye. Wst-1 metabolism values can be used to compensate for small differences in starting cell number. Larger fields can be scanned for visual record of differences.

Those antisense oligonucleotides that result in inhibition of colony formation of SW620 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous colon cells. Those antisense oligonucleotides that inhibit colony formation in SKOV3 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous breast cells. Those antisense oligonucleotides that result in inhibition of colony formation of MDA-MB-231 cells indicate that the corresponding gene plays a role in production or maintenance of the cancerous phenotype in cancerous ovarian cells. Those antisense oligonucleotides that inhibit colony formation in LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells represent genes that play a role in production or maintenance of the cancerous phenotype in cancerous prostate cells.

Example 102: Induction of Cell Death upon Depletion of Polypeptides by Depletion of mRNA ("Antisense Knockout")

In order to assess the effect of depletion of a target message upon cell death, LNCaP, PC3, 22Rv1, MDA-PCA-2b, or DU145 cells, or other cells derived from a cancer of interest, can be transfected for proliferation assays. For cytotoxic effect in the presence of cisplatin (cis), the same protocol is followed but cells are left in the presence of 2 μ M drug. Each day, cytotoxicity is monitored by measuring the amount of LDH enzyme released in the medium

due to membrane damage. The activity of LDH is measured using the Cytotoxicity Detection Kit from Roche Molecular Biochemicals. The data is provided as a ratio of LDH released in the medium vs. the total LDH present in the well at the same time point and treatment (rLDH/tLDH). A positive control using antisense and reverse control oligonucleotides for BCL2 (a known anti-apoptotic gene) is included; loss of message for BCL2 leads to an increase in cell death compared with treatment with the control oligonucleotide (background cytotoxicity due to transfection).

Example 103: Functional Analysis of Gene Products Differentially Expressed in Cancer

The gene products of sequences of a gene differentially expressed in cancerous cells can be further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype. For example, the function of gene products corresponding to genes identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted or associated with a cell surface membrane, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype. In order to generate antibodies, a clone corresponding to a selected gene product is selected, and a sequence that represents a partial or complete coding sequence is obtained. The resulting clone is expressed, the polypeptide produced isolated, and antibodies generated. The antibodies are then combined with cells and the effect upon tumorigenesis assessed.

Where the gene product of the differentially expressed genes identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecules that inhibit or enhance function of the corresponding protein or protein family.

Additional functional assays include, but are not necessarily limited to, those that analyze the effect of expression of the corresponding gene upon cell cycle and cell migration. Methods for performing such assays are well known in the art.

Example 104: Deposit Information.

A deposit of the biological materials in the tables referenced below was made with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, under the provisions of the Budapest Treaty, on or before the filing date of the present application. The accession number indicated is assigned after successful viability testing, and the requisite fees were paid. Access to said cultures will be available during pendency of the patent application to one determined by the Commissioner to be entitled to such under 37 C.F.R. §1.14 and 35 U.S.C. §122. All restriction on availability of said cultures to the public will be irrevocably removed upon the granting of a patent based upon the application. Moreover, the designated deposits will be maintained for a period of thirty (30) years from the date of deposit, or for five (5) years after the last request for the deposit; or for the enforceable life of the U.S. patent, whichever is longer. Should a culture become nonviable or be inadvertently destroyed, or, in the case of plasmid-containing strains, lose its plasmid, it will be replaced with a viable culture(s) of the same taxonomic description.

These deposits are provided merely as a convenience to those of skill in the art, and are not an admission that a deposit is required. A license may be required to make, use, or sell the deposited materials, and no such license is hereby granted. The deposit below was received by the ATCC on or before the filing date of the present application.

Table 155. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4-A	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 156 below provides the ATCC Accession Nos. of the clones deposited as a library named ES217. The deposit was made on January 18, 2001. Table 157 (inserted before the claims) provides the ATCC Accession Nos. of the clones deposited as libraries named ES210-ES216 on July 25, 2000.

Table 156: Clones Deposited as Library No. ES217 with ATCC on or before January 18, 2001.

CloneID	CMCC#	ATCC#	CloneID	CMCC#	ATCC#
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CloneID	CMCC#	ATCC#	CloneID	CMCC#	ATCC#
M00073094B:A01	5418	PTA-2918	M00073425A:H12	5418	PTA-2918
M00073096B:A12	5418	PTA-2918	M00073427B:E04	5418	PTA-2918
M00073412C:E07	5418	PTA-2918	M00073408A:D06	5418	PTA-2918
M00073408C:F06	5418	PTA-2918	M00073428D:H03	5418	PTA-2918
M00073435C:E06	5418	PTA-2918	M00073435B:E11	5418	PTA-2918
M00073403B:F06	5418	PTA-2918	M00074323D:F09	5418	PTA-2918
M00073412D:B07	5418	PTA-2918	M00074333D:A11	5418	PTA-2918
M00073421C:B07	5418	PTA-2918	M00074335A:H08	5418	PTA-2918
M00073429B:H10	5418	PTA-2918	M00074337A:G08	5418	PTA-2918
M00073412D:E02	5418	PTA-2918	M00074340B:D06	5418	PTA-2918
M00073097C:A03	5418	PTA-2918	M00074343C:A03	5418	PTA-2918
M00073403C:C10	5418	PTA-2918	M00074346A:H09	5418	PTA-2918
M00073425D:F08	5418	PTA-2918	M00074347B:F11	5418	PTA-2918
M00073403C:E11	5418	PTA-2918	M00074349A:E08	5418	PTA-2918
M00073431A:G02	5418	PTA-2918	M00074355D:H06	5418	PTA-2918
M00073412A:C03	5418	PTA-2918	M00074361C:B01	5418	PTA-2918
M00073424D:C03	5418	PTA-2918	M00074365A:E09	5418	PTA-2918
M00073430C:A01	5418	PTA-2918	M00074366A:D07	5418	PTA-2918
M00073407A:E12	5418	PTA-2918	M00074366A:H07	5418	PTA-2918
M00073412A:H09	5418	PTA-2918	M00074370D:G09	5418	PTA-2918
M00073418B:B09	5418	PTA-2918	M00074375D:E05	5418	PTA-2918
M00073403C:H09	5418	PTA-2918	M00074382D:F04	5418	PTA-2918
M00073416B:F01	5418	PTA-2918	M00074384D:G07	5418	PTA-2918
M00073425A:G10	5418	PTA-2918	M00074388B:E07	5418	PTA-2918
M00073427B:C08	5418	PTA-2918	M00074392C:D02	5418	PTA-2918
M00073430C:B02	5418	PTA-2918	M00074405B:A04	5418	PTA-2918
M00073418B:H09	5418	PTA-2918	M00074417D:F07	5418	PTA-2918
M00073423C:E01	5418	PTA-2918	M00074392D:D01	5418	PTA-2918
M00074391B:D02	5418	PTA-2918	M00074406B:F10	5418	PTA-2918
M00074390C:E04	5418	PTA-2918	M00074430D:G09	5418	PTA-2918
M00074411B:G07	5418	PTA-2918	M00074395A:B11	5418	PTA-2918
M00074415B:A01	5418	PTA-2918	M00074404B:H01	5418	PTA-2918

Table 157

ES No.	CLONE ID	ATCC#	ES No.	CLONE ID	ATCC#
ES 210	M00073054A:A06	PTA-2376	ES 213	M00074100B:E01	PTA-2379
ES 210	M00073054A:C10	PTA-2376	ES 213	M00074101D:D07	PTA-2379
ES 210	M00073054B:E07	PTA-2376	ES 213	M00074102A:C04	PTA-2379
ES 210	M00073054C:E02	PTA-2376	ES 213	M00074105A:D02	PTA-2379

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ES 212	M00073884D:B06	PTA-2378	ES 215	M00074654D:B05	PTA-2381
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ES 212	M00073891C:A12	PTA-2378	ES 215	M00074662D:D01	PTA-2381
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ES 212	M00073897B:B11	PTA-2378	ES 215	M00074668D:D04	PTA-2381
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ES 212	M00073912B:C04	PTA-2378	ES 215	M00074681D:A02	PTA-2381
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ES 212	M00073967C:A01	PTA-2378	ES 215	M00075043B:H05	PTA-2381
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ES 212	M00073988D:F09	PTA-2378	ES 215	M00075126D:H07	PTA-2381
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ES 212	M00074021C:H07	PTA-2378	ES 216	M00075249A:B08	PTA-2382
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ES 212	M00074024B:G07	PTA-2378	ES 216	M00075255A:G11	PTA-2382
ES 212	M00074025A:F06	PTA-2378	ES 216	M00075259C:G02	PTA-2382
ES 212	M00074025B:A12	PTA-2378	ES 216	M00075270D:A02	PTA-2382
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ES 212	M00074027D:B03	PTA-2378	ES 216	M00075274B:F06	PTA-2382
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ES 212	M00074036D:B05	PTA-2378	ES 216	M00075309C:A06	PTA-2382
ES 212	M00074037A:B03	PTA-2378	ES 216	M00075323B:B12	PTA-2382
ES 212	M00074038A:G08	PTA-2378	ES 216	M00075324B:C10	PTA-2382
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ES 213	M00072944A:C07	PTA-2379	ES 216	M00075365B:B06	PTA-2382

ES 213	M00072944A:E06	PTA-2379	ES 216	M00075384A:B03	PTA-2382
ES 213	M00072944C:C02	PTA-2379	ES 216	M00075389B:C06	PTA-2382
ES 213	M00072944D:C08	PTA-2379	ES 216	M00075391D:D07	PTA-2382
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ES 213	M00072961B:G10	PTA-2379	ES 216	M00075380D:F06	PTA-2382
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ES 213	M00072963B:G11	PTA-2379	ES 216	M00075359D:E09	PTA-2382
ES 213	M00072967A:G07	PTA-2379	ES 216	M00075365D:H01	PTA-2382
ES 213	M00072967B:G06	PTA-2379	ES 216	M00075373C:B09	PTA-2382
ES 213	M00072968A:F08	PTA-2379	ES 216	M00075378B:C07	PTA-2382
ES 213	M00072968D:A06	PTA-2379	ES 216	M00075379A:E07	PTA-2382
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ES 213	M00074075B:A09	PTA-2379	ES 216	M00075454C:D06	PTA-2382
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ES 213	M00074076B:F04	PTA-2379	ES 216	M00075459A:C02	PTA-2382
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			ES 216	M00075609A:H06	PTA-2382
			ES 216	M00075613D:F01	PTA-2382
			ES 216	M00075619C:D08	PTA-2382
			ES 216	M00075621A:F06	PTA-2382
			ES 216	M00075639A:D12	PTA-2382

Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the

art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

EXAMPLE 105:Detection of genes that are differentially expressed in cancer cells

Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues. Table 158

5 (inserted prior to claims) provides information about the polynucleotides on the arrays including: (a) the “SEQ ID”, corresponding to the sequences of the Sequence Listing provided herein; (b) the “SeqName”, corresponding to a internal reference name for the sequence; (c) the “Clone Id”, corresponding to the identifier of a clone from which the sequence is derived; (d) the “Seq Type”, corresponding to the type of the sequence, either interenal or consensus; (e) the
10 “Lib. Name”, corresponding to the library from which the clone was obtained ; (f) the “Cluster Id”, corresponding to an internal identifier for a set of sequences that have been grouped, i.e., clustered, based on their sequence identity, and (g), the “Length”, corresponding to the length of the sequence.

Normal and cancerous tissues were collected from patients using laser capture
15 microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama et al. (2000) Biotechniques 29:530-6; Curran et al. (2000) Mol. Pathol. 53:64-8; Suarez-Quian et al. (1999) Biotechniques 26:328-35; Simone et al. (1998) Trends Genet 14:272-6; Conia et al. (1997) J. Clin. Lab. Anal. 11:28-38; Emmert-Buck et al. (1996) Science 274:998-1001).

20 In general, patients (pats) had breast cancer (brst), prostate cancer (prst), colon cancer (cln). Patients with colon cancer had metastasized colon cancer (met or M), and/or primary tumors (T). Metastases of colon cancers may appear in any tissue, including bone, breast, lung, liver, brain, kidney skin, intestine, appendix, etc. In many patients, the colon cancer had metastasized to liver.

25 cDNA probes were prepared from total RNA isolated from the patient samples described above. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

In most experiments, total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA
30 was then transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, e.g., Luo et al. (1999) Nature Med 5:117-122), and the antisense RNA was then

converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling.

Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from a normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red), and vice versa.

In many experiments, each array used had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots, for a total of about 9,216 spots on each array. The two areas are spotted identically which provides for at least two duplicates of each clone per array.

Polynucleotides for use on the arrays were obtained from both publicly available sources and from cDNA libraries generated from selected cell lines and patient tissues as described. PCR products of from about 0.5kb to 2.0 kb amplified from these sources were spotted onto the array using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides. The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1. For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about four duplicate measurements for each clone, two of one color and two of the other, for each sample. In some experiments Affymetrix oligonucleotide arrays were used.

The differential expression assay was performed by mixing equal amounts of probes from matched or unmatched samples. The arrays were pre-incubated for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC,

and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular
5 Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes
10 repeated with two more slides (one in each color direction). The level of fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of
15 each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-
20 value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the matched or unmatched samples. If the tumor sample has detectable expression and the normal does not, the ratio is
25 truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were
30 populated using a 95% confidence level ($p > 0.05$).

Results

Table 159 provides results obtained according to the methods set forth above. The results show data from several separate experiments using the same set of gene products, each identified by SEQ ID NO. The results for a particular SEQ ID are expressed as a percentage of the total number of patients in which that SEQ ID was over-expressed by at least two fold at a 95% confidence level. Accordingly, for example, SEQ ID NO:23576, the first entry, is expressed in tumor samples of 21.74% (% Brst Pats) of 23 patients (# Brst Pats) with breast cancer.

The six experiments were: 1) a comparison of the gene expression profile of cancerous breast cells to that of normal breast cells (results shown in column 3, entitled "% Brst Pats"), 2) a comparison of the gene expression profile of cancerous colon cells (primary tumor) to that of normal colon cells (results shown in column 5, entitled "% Cln Pats"), 3) a comparison of the gene expression profile of cancerous prostate cells to that of normal prostate cells (results shown in column 7, entitled "% Prst Pats"), 4) a comparison of the gene expression profile of metastasized cancerous colon cells to that of unmatched controls (i.e., a pooled sample of normal colon from many patients; results shown in column 9, entitled "% Cln Unm Met"), 5) a comparison of the gene expression profile of cancerous metastasized colon cells to that of matched (i.e. from the same patient) normal colon cells (results shown in column 11, entitled "% Cln Match met"), and 6) a comparison of the gene expression profile of cancerous metastasized colon cells to that of matched (i.e., from the same patient) colon cancer cells from a primary tumor (results shown in column 13, entitled "% Cln Match Met M/T"). Also shown in Table 159 are "SPOT ID" entries, which correspond to an internal reference identifier.

Table 160 also provides results obtained according to the methods set forth above. The results show data from several separate experiments using the same set of gene products, each identified by SEQ ID NO. Again, the results for a particular SEQ ID are expressed as a percentage of the total number of patients in which that SEQ ID was over-expressed by at least two fold at a 95% confidence level. Accordingly, for example, SEQ ID NO:23569, the first entry, is expressed in breast tumor samples of 24.44% (% Breast T/N $\geq 2x$) of 45 patients Breast T/N patients) with breast cancer.

The two experiments were: 1) a comparison of the gene expression profile of cancerous breast cells (primary tumor) to that of normal breast cells (results shown in column 3, entitled "% Breast T/N $\geq 2x$ "), and 2) a comparison of the gene expression profile of cancerous colon

cells (primary tumor) to that of normal colon cells (results shown in column 5, entitled “% Colon T/N>=2x”). The number of patients in the patient samples are shown in columns 4 and 6. Also shown is a column entitled “PROBESET Id”, which corresponds to an internal reference identifier.

- 5 These data show that the sequences set forth in the in the sequence listing may be used to detect cancerous cells, particularly, cancerous colon, prostate, breast, and metastasized colon cells.

TABLE 158

Seq Id	SeqName	Clone Id	Seq Type	Lib Name	Cluster Id	Length
23569	5059.K19.GZ43_643335	M00079817D:G03	internal	chiron(27)	800071	519
23570	5060.E21.GZ43_643745	M00079848A:B09	internal	chiron(27)	1089548	535
23571	5060.G17.GZ43_643683	M00079856A:C12	internal	chiron(27)	381805	445
23572	5061.A19.gz43_646815	M00079888C:C02	internal	chiron(27)	657028	619
23573	5061.C02.gz43_646545	M00079891C:A07	internal	chiron(27)	1117586	637
23574	5061.E17.gz43_646787	M00079902A:G08	internal	chiron(27)	1116829	499
23575	5061.M03.gz43_646571	M00079929D:E09	internal	chiron(27)	800071	557
23576	5061.N15.gz43_646764	M00079935C:A07	internal	chiron(27)	398438	484
23577	5061.O18.gz43_646813	M00079939B:G07	internal	chiron(27)	774843	635
23578	5061.P08.gz43_646654	M00079940C:D02	internal	chiron(27)	431141	593
23579	5062.M21.GZ43_647243	M00079986C:G03	internal	chiron(27)	42008	541
23580	5063.A16.GZ43_647535	M00079998A:H03	internal	chiron(27)	42008	405
23581	5063.E24.GZ43_647667	M00080010A:G05	internal	chiron(27)	583076	518
23582	5065.G16.GZ43_648309	M00080110D:D02	internal	chiron(27)	1118029	590
23583	5065.P08.GZ43_648190	M00080136D:A10	internal	chiron(27)	807607	274
23584	5184.G17.GZ43_667153	M00082049D:B06	internal	chiron(28)	833900	472
23585	5185.K01.GZ43_667285	M00082099D:D04	internal	chiron(28)	149149	376
23586	5185.L02.GZ43_667302	M00082103C:H08	internal	chiron(28)	416674	329
23587	5185.L12.GZ43_667462	M00082104C:A10	internal	chiron(28)	158514	385
23588	5186.J19.GZ43_667956	M00082152A:B06	internal	chiron(29)	20806	562
23589	5186.J24.GZ43_668036	M00082152B:H01	internal	chiron(29)	1110239	556
23590	5186.N17.GZ43_667928	M00082164D:A10	internal	chiron(29)	410674	476
23591	5188.A08.GZ43_668539	M00082232D:E02	internal	chiron(29)	1118027	546
23592	5188.G06.GZ43_668513	M00082256A:E06	internal	chiron(29)	551209	610

23593	5188.H20.GZ43_668738	M00082263A:F11	internal	chiron(29)	525660	636
23594	5189.O12.GZ43_669001	M00082342A:A11	internal	chiron(29)	480233	606
23595	5189.P10.GZ43_668970	M00082338A:C01	internal	chiron(29)	726873	441
23596	5190.E23.GZ43_669551	M00082382D:C05	internal	chiron(29)	1067312	622
23597	5190.N13.GZ43_669400	M00082417A:E03	internal	chiron(29)	410674	563
23598	5191.G05.GZ43_669649	M00082457B:B05	internal	chiron(29)	25422	497
23599	5193.E14.GZ43_670943	M00082591A:A11	internal	chiron(29)	967199	501
23600	5193.M09.GZ43_670871	M00082618A:G07	internal	chiron(29)	1135172	662
23601	5193.O06.GZ43_670825	M00082628B:F05	internal	chiron(29)	17174	524
23602	5195.C15.GZ43_671725	M00082718D:E03	internal	chiron(29)	400889	613
23603	5195.E15.GZ43_671727	M00082729C:C08	internal	chiron(29)	1193184	602
23604	5234.B09.GZ43_673764	M00083298C:G12	internal	chiron(29)	1119238	497
23605	5234.H23.GZ43_673994	M00083332C:D11	internal	chiron(29)	25422	644
23606	5234.O05.GZ43_673713	M00083289D:G08	internal	chiron(29)	583076	624
23607	5236.J03.GZ43_674444	M00083437D:E04	internal	chiron(29)	606382	426
23608	5236.O18.GZ43_674689	M00083459D:B01	internal	chiron(29)	378206	580
23609	5238.A24.GZ43_675194	M00083524A:G10	internal	chiron(29)	726873	473
23610	Clu1052434.con_1		consensus		1052434	352
23611	Clu1052615.con_1		consensus		1052615	439
23612	Clu1053096.con_1		consensus		1053096	529
23613	Clu1058283.con_1		consensus		1058283	824
23614	Clu1067312.con_1		consensus		1067312	691
23615	Clu1069553.con_2		consensus		1069553	576
23616	Clu1080217.con_1		consensus		1080217	547
23617	Clu1081611.con_1		consensus		1081611	399
23618	Clu1082099.con_1		consensus		1082099	440
23619	Clu1082189.con_1		consensus		1082189	470
23620	Clu1082283.con_2		consensus		1082283	529
23621	Clu1082399.con_1		consensus		1082399	534
23622	Clu1082489.con_1		consensus		1082489	355
23623	Clu1082628.con_1		consensus		1082628	554
23624	Clu1082731.con_1		consensus		1082731	289
23625	Clu1083148.con_1		consensus		1083148	757
23626	Clu1083900.con_1		consensus		1083900	502
23627	Clu1089548.con_1		consensus		1089548	667
23628	Clu1116089.con_1		consensus		1116089	369

23629	Clu1116829.con_1		consensus		1116829	586
23630	Clu1116919.con_1		consensus		1116919	806
23631	Clu1116945.con_1		consensus		1116945	566
23632	Clu1117021.con_1		consensus		1117021	978
23633	Clu1117079.con_1		consensus		1117079	543
23634	Clu1117586.con_1		consensus		1117586	678
23635	Clu1117625.con_1		consensus		1117625	277
23636	Clu1118027.con_1		consensus		1118027	590
23637	Clu1118511.con_1		consensus		1118511	815
23638	Clu1119238.con_1		consensus		1119238	588
23639	Clu1119896.con_1		consensus		1119896	386
23640	Clu1126645.con_1		consensus		1126645	509
23641	Clu1132147.con_1		consensus		1132147	583
23642	Clu1139444.con_1		consensus		1139444	677
23643	Clu1139499.con_1		consensus		1139499	498
23644	Clu1140276.con_1		consensus		1140276	485
23645	Clu1140367.con_2		consensus		1140367	424
23646	Clu1140589.con_1		consensus		1140589	821
23647	Clu1141931.con_1		consensus		1141931	565
23648	Clu1193580.con_1		consensus		1193580	629
23649	Clu1193799.con_1		consensus		1193799	733
23650	Clu1193833.con_2		consensus		1193833	566
23651	Clu149149.con_2		consensus		149149	564
23652	Clu19522.con_1		consensus		19522	809
23653	Clu21222.con_1		consensus		21222	774
23654	Clu25422.con_1		consensus		25422	766
23655	Clu258716.con_1		consensus		258716	872
23656	Clu374843.con_1		consensus		374843	656
23657	Clu377719.con_1		consensus		377719	1382
23658	Clu377939.con_1		consensus		377939	1152
23659	Clu378206.con_1		consensus		378206	584
23660	Clu398438.con_1		consensus		398438	736
23661	Clu400889.con_1		consensus		400889	741
23662	Clu403038.con_1		consensus		403038	773
23663	Clu410674.con_1		consensus		410674	822
23664	Clu411226.con_1		consensus		411226	907

23665	Clu413700.con_1		consensus		413700	951
23666	Clu416674.con_1		consensus		416674	766
23667	Clu42008.con_1		consensus		42008	1057
23668	Clu451094.con_1		consensus		451094	443
23669	Clu451310.con_1		consensus		451310	484
23670	Clu451496.con_2		consensus		451496	1000
23671	Clu455524.con_1		consensus		455524	363
23672	Clu456861.con_1		consensus		456861	525
23673	Clu480233.con_2		consensus		480233	622
23674	Clu512287.con_2		consensus		512287	491
23675	Clu525660.con_1		consensus		525660	650
23676	Clu532281.con_1		consensus		532281	636
23677	Clu552745.con_1		consensus		552745	373
23678	Clu554732.con_1		consensus		554732	474
23679	Clu556189.con_1		consensus		556189	698
23680	Clu579754.con_1		consensus		579754	653
23681	Clu593641.con_1		consensus		593641	890
23682	Clu643318.con_1		consensus		643318	498
23683	Clu657028.con_1		consensus		657028	807
23684	5072.K10.GZ43_650909	M00080470D:C10	internal	chiron(27)	410674	557
23685	5072.P20.GZ43_651074	M00080489D:G10	internal	chiron(27)	856078	489
23686	5073.C07.GZ43_651237	M00080495C:B05	internal	chiron(27)	533096	590
23687	5073.D08.GZ43_651254	M00080498D:E12	internal	chiron(27)	1067312	578
23688	5073.J20.GZ43_651452	M00080515D:H06	internal	chiron(27)	400889	504
23689	5074.H06.GZ43_651610	M00080558A:G02	internal	chiron(27)	618862	544
23690	5074.J21.GZ43_651852	M00080569D:E04	internal	chiron(27)	1118511	573
23691	5075.A20.GZ43_652211	M00080608C:E03	internal	chiron(27)	1117586	584
23692	5075.M03.GZ43_651951	M00080642C:G04	internal	chiron(27)	723800	577
23693	5076.B04.GZ43_652340	M00080658D:B05	internal	chiron(27)	1083148	615
23694	5076.H07.GZ43_652394	M00080683A:F07	internal	chiron(27)	168428	548
23695	5076.P22.GZ43_652642	M00080721A:B11	internal	chiron(27)	1118511	625
23696	5097.D01.GZ43_652699	M00080728C:A06	internal	chiron(27)	1116829	533
23697	5097.M04.GZ43_652756	M00080734D:A04	internal	chiron(27)	613936	565
23698	5097.P10.GZ43_652855	M00080747A:B06	internal	chiron(27)	831704	195
23699	5098.C09.GZ43_653210	M00080839A:C05	internal	chiron(27)	1117079	536
23700	5098.E12.GZ43_653260	M00080849C:A06	internal	chiron(27)	666002	500

23701	5130.F02.GZ43_659697	M00081454C:B02	internal	chiron(28)	833900	670
23702	5130.O17.GZ43_659946	M00081478A:A12	internal	chiron(28)	520284	542
23703	5130.P09.GZ43_659819	M00081479D:H03	internal	chiron(28)	1138736	621
23704	5131.N24.GZ43_660441	M00081516A:F04	internal	chiron(28)	469630	455
23705	5132.D09.GZ43_660575	M00081524D:E12	internal	chiron(28)	411226	558
23706	5133.B13.GZ43_661021	M00081558D:C08	internal	chiron(28)	532281	415
23707	5133.G11.GZ43_660994	M00081568D:D02	internal	chiron(28)	89239	557
23708	5133.J24.GZ43_661205	M00081574B:A04	internal	chiron(28)	644751	550
23709	5133.N07.GZ43_660937	M00081580D:E03	internal	chiron(28)	526675	603
23710	5134.J13.GZ43_661413	M00081607C:D05	internal	chiron(28)	964646	489
23711	5134.N11.GZ43_661385	M00081616B:H01	internal	chiron(28)	454662	397
23712	5134.O05.GZ43_661290	M00081618A:B06	internal	chiron(28)	31223	491
23713	5136.B15.GZ43_662228	M00081661D:A10	internal	chiron(28)	1069553	413
23714	5136.H18.GZ43_662282	M00081678A:A12	internal	chiron(28)	512287	487
23715	5136.K03.GZ43_662045	M00081683B:C09	internal	chiron(28)	532281	626
23716	5136.K16.GZ43_662253	M00081684B:C10	internal	chiron(28)	378206	509
23717	5136.P01.GZ43_662018	M00081693B:F12	internal	chiron(28)	89239	495
23718	Clu666002.con_1		consensus		666002	530
23719	Clu685022.con_1		consensus		685022	599
23720	Clu715440.con_2		consensus		715440	611
23721	Clu726873.con_1		consensus		726873	687
23722	Clu775364.con_1		consensus		775364	601
23723	Clu800071.con_1		consensus		800071	685
23724	Clu807607.con_1		consensus		807607	562
23725	Clu954632.con_1		consensus		954632	292
23726	Clu964646.con_1		consensus		964646	526
23727	Clu982132.con_1		consensus		982132	987
23728	5066.J20.GZ43_648760	M00080164D:H10	internal	chiron(27)	618862	344
23729	5066.N15.GZ43_648684	M00080179D:G07	internal	chiron(27)	1083148	259
23730	5066.O24.GZ43_648829	M00080184B:C10	internal	chiron(27)	19522	303
23731	5069.A20.GZ43_649907	M00080285A:E12	internal	chiron(27)	1119238	588
23732	5069.I09.GZ43_649739	M00080317A:G01	internal	chiron(27)	1117079	537
23733	5069.M04.GZ43_649663	M00080331C:D09	internal	chiron(27)	685022	592
23734	5070.G07.GZ43_650089	M00080362D:F11	internal	chiron(27)	258716	520
23735	5071.H06.GZ43_650458	M00080407D:G09	internal	chiron(27)	386188	216
23736	5071.J11.GZ43_650540	M00080413D:D07	internal	chiron(27)	1117021	569

23737	5098.I02.GZ43_653104	M00080819B:G07	internal	chiron(27)	398438	459
23738	5101.B10.GZ43_654377	M00081030A:D09	internal	chiron(28)	1139444	562
23739	5102.A22.GZ43_654952	M00081093B:C04	internal	chiron(28)	1139037	467
23740	5103.J01.GZ43_655009	M00081178D:C12	internal	chiron(28)	643318	455
23741	5104.I13.GZ43_655584	M00081223D:D06	internal	chiron(28)	558521	637
23742	5104.O16.GZ43_655638	M00081228B:C04	internal	chiron(28)	1139048	327
23743	5105.P13.GZ43_655975	M00081288D:G08	internal	chiron(28)	1140612	542
23744	5106.I21.GZ43_656480	M00081313D:B12	internal	chiron(28)	643318	498
23745	5106.M18.GZ43_656436	M00081323D:C07	internal	chiron(28)	964646	429
23746	5127.A11.GZ43_658684	M00081333C:A04	internal	chiron(28)	89239	438
23747	5127.E23.GZ43_658880	M00081344A:C10	internal	chiron(28)	715440	610
23748	5128.J24.GZ43_659285	M00081385B:D11	internal	chiron(28)	848070	546
23749	5128.L10.GZ43_659063	M00081388B:A12	internal	chiron(28)	1138291	483
23750	5129.J16.GZ43_659541	M00081428A:B10	internal	chiron(28)	1141931	482
23751	5129.P04.GZ43_659355	M00081441D:F01	internal	chiron(28)	1117586	496
23752	5130.C16.GZ43_659918	M00081450C:E09	internal	chiron(28)	523988	573
23753	5130.D14.GZ43_659887	M00081452A:G03	internal	chiron(28)	631472	408
23754	5177.B11.GZ43_664364	M00081717D:A10	internal	chiron(28)	411226	366
23755	5177.D13.GZ43_664398	M00081723A:C02	internal	chiron(28)	1139444	493
23756	5177.H05.GZ43_664274	M00081705D:B04	internal	chiron(28)	964646	406
23757	5178.G24.GZ43_664961	M00081767C:G04	internal	chiron(28)	374843	614
23758	5178.N01.GZ43_664600	M00081780B:F07	internal	chiron(28)	884215	516
23759	5179.I06.GZ43_665059	M00081806D:C10	internal	chiron(28)	685022	593
23760	5179.L07.GZ43_665078	M00081812D:A11	internal	chiron(28)	9087	444
23761	5181.B17.GZ43_665996	M00081873D:A03	internal	chiron(28)	1117625	129
23762	5181.C18.GZ43_666013	M00081878B:G04	internal	chiron(28)	512287	434
23763	5181.O23.GZ43_666105	M00081914C:H06	internal	chiron(28)	1140589	509
23764	5182.L02.GZ43_666150	M00081924D:E02	internal	chiron(28)	532281	627
23765	5182.M10.GZ43_666279	M00081938B:D03	internal	chiron(28)	480233	618
23766	5183.J06.GZ43_666596	M00081995C:C03	internal	chiron(28)	867272	521
23767	5183.K20.GZ43_666821	M00081999D:H07	internal	chiron(28)	416674	394

TABLE 159

SEQ ID	SPOT ID	% Brst Pats	# Brst Pats	% Cln Pats	# Cln Pats	% Prst Pats	# Prst Pats	% Cln Unm Met	# Cln Unm Met Pats	% Cln Match Met	# Cln Match Met M/N Pats	% Cln Match Met M/T	% Cln Match Met M/T
23576	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23576	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23577	42089	13.04	23	23.68	76	9.80	102	3.03	33	8.33	36		36
23579	10592		23	24.68	77		102	12.12	33	16.67	36		36
23579	10592		23	24.68	77		102	12.12	33	16.67	36		36
23580	10592		23	24.68	77		102	12.12	33	16.67	36		36
23581	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23584	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23585	62233	30.43	23	31.58	19	7.22	97			16.67	18	5.56	18
23585	53177	30.43	23	20.00	75	7.84	102	30.30	33	28.57	35	5.56	36
23585	62233	30.43	23	31.58	19	7.22	97			16.67	18	5.56	18
23586	61035	17.39	23	15.79	19	22.68	97			5.56	18		18
23586	61035	17.39	23	15.79	19	22.68	97			5.56	18		18
23588	65344	21.74	23	31.58	19		97			16.67	18		18
23588	65344	21.74	23	31.58	19		97			16.67	18		18
23588	65344	21.74	23	31.58	19		97			16.67	18		18
23588	61198	21.74	23	10.53	19	2.06	97			11.11	18		18
23588	61198	21.74	23	10.53	19	2.06	97			11.11	18		18
23594	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23594	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23596	62019	30.43	23		19		97				18		18
23596	62019	30.43	23		19		97				18		18
23598	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23598	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23599	3835		8	20.00	35	2.94	34	23.33	30	14.29	7		7
23601	3835		8	20.00	35	2.94	34	23.33	30	14.29	7		7
23602	35056	4.35	23	30.67	75	1.96	102	54.55	33	36.11	36		36
23603	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23603	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23605	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23605	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23605	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23605	61000	26.09	23	5.26	19	32.99	97				18	16.67	18

23606	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23607	65474	21.74	23	78.95	19	12.37	97			66.67	18		18
23607	65474	21.74	23	78.95	19	12.37	97			66.67	18		18
23614	62019	30.43	23		19		97				18		18
23614	62019	30.43	23		19		97				18		18
23615	51042	26.09	23	2.67	75	3.92	102	3.03	33		35		36
23615	51042	26.09	23	2.67	75	3.92	102	3.03	33		35		36
23630	37575	4.35	23	22.67	75	14.71	102		33	36.11	36	5.56	36
23630	37575	4.35	23	22.67	75	14.71	102		33	36.11	36	5.56	36
23646	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23646	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23646	46009		23	30.26	76	8.82	102	21.21	33	51.43	35	5.56	36
23646	4066		8	28.57	35	11.76	34	26.67	30	42.86	7		7
23646	4066		8	28.57	35	11.76	34	26.67	30	42.86	7		7
23646	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23651	53177	30.43	23	20.00	75	7.84	102	30.30	33	28.57	35	5.56	36
23651	62233	30.43	23	31.58	19	7.22	97			16.67	18	5.56	18
23651	62233	30.43	23	31.58	19	7.22	97			16.67	18	5.56	18
23651	54930	21.74	23	16.00	75	9.80	102	21.21	33	25.71	35		36
23654	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23654	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23654	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23654	61000	26.09	23	5.26	19	32.99	97				18	16.67	18
23656	60741		23	47.37	19	22.68	97			33.33	18		18
23660	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23660	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23661	35056	4.35	23	30.67	75	1.96	102	54.55	33	36.11	36		36
23666	61035	17.39	23	15.79	19	22.68	97			5.56	18		18
23666	61035	17.39	23	15.79	19	22.68	97			5.56	18		18
23667	10592		23	24.68	77		102	12.12	33	16.67	36		36
23667	10592		23	24.68	77		102	12.12	33	16.67	36		36
23673	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23673	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23676	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23679	52789	17.39	23	6.67	75	4.90	102	21.21	33	8.57	35		36
23681	35754		23	20.00	75	2.94	102	30.30	33	36.11	36		36

23681	36946		23	24.00	75	1.96	102	18.18	33	30.56	36	2.78	36
23681	35754		23	20.00	75	2.94	102	30.30	33	36.11	36		36
23681	36946		23	24.00	75	1.96	102	18.18	33	30.56	36	2.78	36
23681	34559		23	30.67	75	1.96	102	30.30	33	33.33	36	5.56	36
23687	62019	30.43	23		19		97				18		18
23687	62019	30.43	23		19		97				18		18
23688	35056	4.35	23	30.67	75	1.96	102	54.55	33	36.11	36		36
23698	65508	30.43	23		19	12.37	97				18		18
23698	35939	26.09	23		75	9.80	102		33	8.33	36		36
23698	55189	26.09	23	5.26	19	8.16	98				17		18
23698	65508	30.43	23		19	12.37	97				18		18
23698	54046	26.09	23		75	14.71	102	3.03	33		35	2.78	36
23700	62439	21.74	23		19		97				18		18
23700	62439	21.74	23		19		97				18		18
23701	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23702	61479	26.09	23	63.16	19	3.09	97			61.11	18		18
23702	33688	17.39	23	21.05	76	0.98	102	15.15	33	34.29	35	2.78	36
23702	54586	17.39	23	12.00	75		102	6.06	33	31.43	35		36
23702	51783	21.74	23	38.67	75	1.96	102	30.30	33	57.14	35		36
23702	17831	22.22	18	39.02	41	1.56	64	40.00	30	54.55	11	9.09	11
23704	60458	4.35	23	57.89	19	25.77	97			61.11	18		18
23704	60458	4.35	23	57.89	19	25.77	97			61.11	18		18
23704	60458	4.35	23	57.89	19	25.77	97			61.11	18		18
23704	60458	4.35	23	57.89	19	25.77	97			61.11	18		18
23706	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23707	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23712	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23713	51042	26.09	23	2.67	75	3.92	102	3.03	33		35		36
23713	51042	26.09	23	2.67	75	3.92	102	3.03	33		35		36
23715	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23717	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23718	62439	21.74	23		19		97				18		18
23718	62439	21.74	23		19		97				18		18
23719	9191	21.74	23	55.84	77	3.92	102	39.39	33	58.33	36	11.11	36
23727	11583	21.74	23	44.16	77	1.96	102	27.27	33	66.67	36	2.78	36
23727	37868	26.09	23	49.33	75	4.90	102	36.36	33	55.56	36	5.56	36

23727	37868	26.09	23	49.33	75	4.90	102	36.36	33	55.56	36	5.56	36
23727	35285	30.43	23	56.00	75	2.94	102	33.33	33	52.78	36	8.33	36
23727	35285	30.43	23	56.00	75	2.94	102	33.33	33	52.78	36	8.33	36
23727	11583	21.74	23	44.16	77	1.96	102	27.27	33	66.67	36	2.78	36
23733	9191	21.74	23	55.84	77	3.92	102	39.39	33	58.33	36	11.11	36
23737	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23737	62615	21.74	23	15.79	19		97			5.56	18	5.56	18
23741	63119	26.09	23		19	1.03	97				18	22.22	18
23741	63119	26.09	23		19	1.03	97				18	22.22	18
23746	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23749	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23757	60741		23	47.37	19	22.68	97			33.33	18		18
23759	9191	21.74	23	55.84	77	3.92	102	39.39	33	58.33	36	11.11	36
23761	64570	4.35	23		19	20.62	97			5.56	18	16.67	18
23761	64570	4.35	23		19	20.62	97			5.56	18	16.67	18
23763	4066		8	28.57	35	11.76	34	26.67	30	42.86	7		7
23763	4066		8	28.57	35	11.76	34	26.67	30	42.86	7		7
23763	46009		23	30.26	76	8.82	102	21.21	33	51.43	35	5.56	36
23763	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23763	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23763	1542		8	54.29	35	20.59	34	40.00	30	57.14	7		7
23764	24511		23	9.38	64	4.00	100	24.24	33	26.09	23	4.35	23
23765	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23765	24403	8.70	23	40.63	64	4.00	100	48.48	33	43.48	23		23
23767	61035	17.39	23	15.79	19	22.68	97			5.56	18		18
23767	61035	17.39	23	15.79	19	22.68	97			5.56	18		18

TABLE 160

Seq Id	PROBESET Id	% Breast T/N >=2x	Breast T/N Patients	% Colon M/N >=2x	Colon M/N Patients
23569	3323	24.44	45	44.83	29
23570	47141	100.00	12	100.00	11
23571	22807	20.83	48	100.00	23
23572	47166	100.00	3	8.33	12
23573	47170	100.00	7	100.00	10

23573	47170	100.00	7	100.00	10
23573	47170	100.00	7	100.00	10
23574	54439	100.00	1		15
23575	3323	24.44	45	44.83	29
23578	47204	100.00	21		27
23581	7337	16.67	18	100.00	14
23582	9348	52.27	44	9.52	21
23583	55586	100.00	4	100.00	4
23584	7337	16.67	18	100.00	14
23587	48770	100.00	3	21.43	28
23589	26738	56.00	25		
23589	26738	56.00	25		
23589	26738	56.00	25		
23589	26738	56.00	25		
23590	48850	4.00	25	50.00	4
23591	35733	100.00	1	77.27	22
23591	35733	100.00	1	77.27	22
23592	25507	100.00	22	18.52	27
23593	48810	100.00	4		28
23595	35493	48.00	50	3.45	29
23595	35493	48.00	50	3.45	29
23596	55391	16.28	43	100.00	1
23597	48850	4.00	25	50.00	4
23600	48901	10.00	20	100.00	11
23600	48901	10.00	20	100.00	11
23604	47395	100.00	1		
23606	7337	16.67	18	100.00	14
23608	35013		44	100.00	10
23608	35013		44	100.00	10
23609	35493	48.00	50	3.45	29
23609	35493	48.00	50	3.45	29
23610	15407	100.00	24	3.85	26
23610	15407	100.00	24	3.85	26
23610	15407	100.00	24	3.85	26
23610	15407	100.00	24	3.85	26
23611	15407	100.00	24	3.85	26

23611	15407	100.00	24	3.85	26
23611	15407	100.00	24	3.85	26
23611	15407	100.00	24	3.85	26
23612	15407	100.00	24	3.85	26
23612	15407	100.00	24	3.85	26
23612	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23613	15407	100.00	24	3.85	26
23614	55391	16.28	43	100.00	1
23616	15407	100.00	24	3.85	26
23616	15407	100.00	24	3.85	26
23616	15407	100.00	24	3.85	26
23616	15407	100.00	24	3.85	26
23617	15407	100.00	24	3.85	26
23617	15407	100.00	24	3.85	26
23617	15407	100.00	24	3.85	26
23618	15407	100.00	24	3.85	26
23618	15407	100.00	24	3.85	26
23618	15407	100.00	24	3.85	26
23618	15407	100.00	24	3.85	26
23618	15407	100.00	24	3.85	26
23619	15407	100.00	24	3.85	26
23619	15407	100.00	24	3.85	26
23619	15407	100.00	24	3.85	26
23619	15407	100.00	24	3.85	26
23619	15407	100.00	24	3.85	26
23620	15407	100.00	24	3.85	26
23620	15407	100.00	24	3.85	26
23620	15407	100.00	24	3.85	26
23620	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26

23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23621	15407	100.00	24	3.85	26
23622	15407	100.00	24	3.85	26
23622	15407	100.00	24	3.85	26
23623	15407	100.00	24	3.85	26
23623	15407	100.00	24	3.85	26
23623	15407	100.00	24	3.85	26
23623	15407	100.00	24	3.85	26
23623	15407	100.00	24	3.85	26
23624	15407	100.00	24	3.85	26
23624	15407	100.00	24	3.85	26
23624	15407	100.00	24	3.85	26
23624	15407	100.00	24	3.85	26
23625	14582	100.00	5	42.86	28
23625	14582	100.00	5	42.86	28
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23626	15407	100.00	24	3.85	26
23627	47141	100.00	12	100.00	11
23628	15407	100.00	24	3.85	26
23628	15407	100.00	24	3.85	26
23628	15407	100.00	24	3.85	26
23628	15407	100.00	24	3.85	26
23629	54439	100.00	1		15
23631	15407	100.00	24	3.85	26
23631	15407	100.00	24	3.85	26
23631	15407	100.00	24	3.85	26
23631	15407	100.00	24	3.85	26

23631	15407	100.00	24	3.85	26
23632	3323	24.44	45	44.83	29
23633	47409			50.00	4
23634	47170	100.00	7	100.00	10
23634	47170	100.00	7	100.00	10
23634	47170	100.00	7	100.00	10
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23635	15407	100.00	24	3.85	26
23636	35733	100.00	1	77.27	22
23636	35733	100.00	1	77.27	22
23637	47589	46.51	43	9.09	22
23638	47395	100.00	1		
23639	15407	100.00	24	3.85	26
23639	15407	100.00	24	3.85	26
23639	15407	100.00	24	3.85	26
23639	15407	100.00	24	3.85	26
23640	15407	100.00	24	3.85	26
23640	15407	100.00	24	3.85	26
23640	15407	100.00	24	3.85	26
23640	15407	100.00	24	3.85	26
23641	15407	100.00	24	3.85	26
23641	15407	100.00	24	3.85	26
23641	15407	100.00	24	3.85	26
23641	15407	100.00	24	3.85	26
23642	52781	100.00	19		27
23643	15407	100.00	24	3.85	26
23643	15407	100.00	24	3.85	26
23643	15407	100.00	24	3.85	26
23643	15407	100.00	24	3.85	26
23643	15407	100.00	24	3.85	26
23644	15407	100.00	24	3.85	26
23644	15407	100.00	24	3.85	26

23644	15407	100.00	24	3.85	26
23644	15407	100.00	24	3.85	26
23645	15407	100.00	24	3.85	26
23645	15407	100.00	24	3.85	26
23645	15407	100.00	24	3.85	26
23647	22180	100.00	5		
23647	22180	100.00	5		
23648	15407	100.00	24	3.85	26
23648	15407	100.00	24	3.85	26
23648	15407	100.00	24	3.85	26
23648	15407	100.00	24	3.85	26
23648	15407	100.00	24	3.85	26
23648	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23649	15407	100.00	24	3.85	26
23650	15407	100.00	24	3.85	26
23650	15407	100.00	24	3.85	26
23650	15407	100.00	24	3.85	26
23650	15407	100.00	24	3.85	26
23652	26408	16.00	50	56.00	25
23652	26408	16.00	50	56.00	25
23653	19860	16.33	49	65.52	29
23655	47444		44	74.07	27
23657	38650	24.14	29	100.00	1
23657	38650	24.14	29	100.00	1
23658	29692	100.00	12		16
23658	29692	100.00	12		16
23659	35013		44	100.00	10
23659	35013		44	100.00	10
23662	47338	100.00	2	25.00	4
23663	48850	4.00	25	50.00	4
23664	54961	100.00	28	7.14	28

23665	26394	68.00	50	34.48	29
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23668	15407	100.00	24	3.85	26
23669	15407	100.00	24	3.85	26
23669	15407	100.00	24	3.85	26
23669	15407	100.00	24	3.85	26
23670	15407	100.00	24	3.85	26
23670	15407	100.00	24	3.85	26
23671	15407	100.00	24	3.85	26
23671	15407	100.00	24	3.85	26
23671	15407	100.00	24	3.85	26
23672	15407	100.00	24	3.85	26
23672	15407	100.00	24	3.85	26
23672	15407	100.00	24	3.85	26
23672	15407	100.00	24	3.85	26
23672	15407	100.00	24	3.85	26
23674	55038	100.00	8	6.67	15
23675	48810	100.00	4		28
23677	15407	100.00	24	3.85	26
23677	15407	100.00	24	3.85	26
23677	15407	100.00	24	3.85	26
23678	15407	100.00	24	3.85	26
23678	15407	100.00	24	3.85	26
23678	15407	100.00	24	3.85	26
23678	15407	100.00	24	3.85	26
23680	47668	39.53	43	50.00	28
23682	47958		42	77.78	27
23683	47166	100.00	3	8.33	12

23718	52866	18.18	44	87.50	8
23719	3323	24.44	45	44.83	29
23720	48070	100.00	2	16.67	18
23721	35493	48.00	50	3.45	29
23721	35493	48.00	50	3.45	29
23722	15407	100.00	24	3.85	26
23722	15407	100.00	24	3.85	26
23722	15407	100.00	24	3.85	26
23722	15407	100.00	24	3.85	26
23722	15407	100.00	24	3.85	26
23723	3323	24.44	45	44.83	29
23724	55586	100.00	4	100.00	4
23725	15407	100.00	24	3.85	26
23725	15407	100.00	24	3.85	26
23725	15407	100.00	24	3.85	26
23725	15407	100.00	24	3.85	26
23725	15407	100.00	24	3.85	26
23725	15407	100.00	24	3.85	26
23726	48510	100.00	6	3.57	28
23728	28027	26.09	46	4.35	23
23728	28027	26.09	46	4.35	23
23729	14582	100.00	5	42.86	28
23729	14582	100.00	5	42.86	28
23730	26408	16.00	50	56.00	25
23731	47395	100.00	1		
23732	47409			50.00	4
23733	3323	24.44	45	44.83	29
23734	47444		44	74.07	27
23735	22963			100.00	1
23736	3323	24.44	45	44.83	29
23684	48850	4.00	25	50.00	4
23685	20206	100.00	4		22
23686	35206		47	100.00	2
23687	55391	16.28	43	100.00	1
23689	28027	26.09	46	4.35	23
23689	28027	26.09	46	4.35	23
23689	28027	26.09	46	4.35	23

23690	47589	46.51	43	9.09	22
23691	47170	100.00	7	100.00	10
23691	47170	100.00	7	100.00	10
23692	47615	34.09	44	100.00	17
23693	14582	100.00	5	42.86	28
23693	14582	100.00	5	42.86	28
23694	47644	100.00	6	25.93	27
23695	47589	46.51	43	9.09	22
23696	54439	100.00	1		15
23697	47682	31.58	19	50.00	16
23697	47682	31.58	19	50.00	16
23699	47409			50.00	4
23700	52866	18.18	44	87.50	8
23738	52781	100.00	19		27
23739	3308	50.00	16		29
23740	47958		42	77.78	27
23742	47958		42	77.78	27
23743	9939	100.00	2		29
23744	47958		42	77.78	27
23745	48510	100.00	6	3.57	28
23746	7337	16.67	18	100.00	14
23747	48070	100.00	2	16.67	18
23748	48510	100.00	6	3.57	28
23749	7337	16.67	18	100.00	14
23750	22180	100.00	5		
23750	22180	100.00	5		
23751	47170	100.00	7	100.00	10
23751	47170	100.00	7	100.00	10
23752	35682	100.00	6		29
23753	48220	100.00	6	3.57	28
23701	7337	16.67	18	100.00	14
23703	48261	100.00	3	100.00	1
23705	54961	100.00	28	7.14	28
23707	7337	16.67	18	100.00	14
23708	54795	100.00	1	100.00	1
23709	52709	100.00	4	100.00	4

23710	48510	100.00	6	3.57	28
23711	4308			100.00	2
23714	55038	100.00	8	6.67	15
23716	35013		44	100.00	10
23716	35013		44	100.00	10
23754	54961	100.00	28	7.14	28
23755	52781	100.00	19		27
23756	48510	100.00	6	3.57	28
23758	19201		30	44.44	9
23759	3323	24.44	45	44.83	29
23760	48580	100.00	4		26
23762	55038	100.00	8	6.67	15
23766	48716			100.00	6

Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.